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OM protein - protein search, using SW model

Run on: March 18, 2004, 07:17:04 ; Search time 33.5 Seconds
(without alignments)
77.300 Million cell updates/sec

Title: US-09-909-348-1

Perfect score: 59

Sequence: 1 CEGDGGFPV 10

Scoring table: BLOSUM62

Gapped 10.0 , Gapext 0.5

Searched: 1049977 seqs, 25895539 residues

Total number of hits satisfying chosen parameters: 32147

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Published Applications AA:*

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Published Applications AA:*

- 1: /cgnd_6_ptodata/_1/pubpaas/_007_PUBCCOMB_Pep:*
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- 18: /cgnd_6_ptodata/_1/pubpaas/_060_PUBCCOMB_Pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	9 US-09-909-348-1	Sequence 1, Appli
2	59	100.0	10	9 US-09-909-122-1	Sequence 1, Appli
3	59	100.0	10	13 US-10-050-682-1	Sequence 1, Appli
4	59	100.0	10	13 US-10-050-682-1	Sequence 1, Appli
5	46	78.0	10	9 US-09-909-348-2	Sequence 2, Appli
6	46	78.0	10	9 US-09-909-122-2	Sequence 2, Appli
7	46	78.0	10	13 US-10-050-682-2	Sequence 2, Appli
8	46	78.0	10	13 US-10-050-682-2	Sequence 2, Appli
9	34	57.6	10	10 US-09-972-404B-606	Sequence 606, App
10	28	47.5	10	10 US-09-572-404B-3584	Sequence 3584, App
11	27	45.8	10	10 US-09-572-404B-3784	Sequence 3784, App
12	27	45.8	10	10 US-09-572-404B-3785	Sequence 3785, App
13	25	42.4	10	9 US-09-879-957-55	Sequence 55, Appli
14	25	42.4	10	10 US-09-572-404B-51	Sequence 51, Appli
15	25	42.4	10	10 US-09-572-404B-53	Sequence 53, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ID	SEQ ID NO	TYPE	LENGTH	ORGANISM	FEATURE	OTHER INFORMATION
1	1	PRT	10	Janet Stierberg	Artificial Sequence	US-09-909-348-1
2	1	PRT	10	Bergmann, John	Stimulation Of Cartilage Growth With Agonists	US-09-909-348-1
3	1	PRT	10	Carney, Darrell H.	GENERAL INFORMATION:	US-09-909-348-1
4	1	PRT	10	Crowther, Roger S.	APPLICANT:	US-09-909-348-1
5	1	PRT	10	Stierberg, Janet	APPLICANT:	US-09-909-348-1
6	1	PRT	10	Bergmann, John	TITLE OF INVENTION:	US-09-909-348-1
7	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
8	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
9	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
10	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
11	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
12	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
13	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
14	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
15	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
16	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
17	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
18	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
19	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
20	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
21	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
22	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
23	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
24	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
25	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
26	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
27	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
28	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
29	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
30	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
31	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
32	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
33	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
34	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
35	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
36	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
37	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
38	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
39	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
40	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
41	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
42	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1
43	1	PRT	10	Carney, Darrell H.	TITLE OF INVENTION:	US-09-909-348-1
44	1	PRT	10	Crowther, Roger S.	TITLE OF INVENTION:	US-09-909-348-1
45	1	PRT	10	Stierberg, Janet	TITLE OF INVENTION:	US-09-909-348-1

Sequence 55, Appli
Sequence 63, Appli
Sequence 174, Appli
Sequence 2027, Appli
Sequence 2033, Appli
Sequence 2091, Appli
Sequence 2093, Appli
Sequence 2095, Appli
Sequence 2798, Appli
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Sequence 285, Appli
Sequence 293, Appli
Sequence 299, Appli
Sequence 345, Appli
Sequence 58, Appli
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Sequence 592-58
Sequence 114, Appli
Sequence 114-114
Sequence 176, Appli
Sequence 342, Appli
Sequence 344, Appli
Sequence 345, Appli
SEQ ID NO 1

LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Peptide fragment of Thrombin
OTHER INFORMATION: Peptide fragment of Thrombin

RESULT 1
US-09-909-348-1
Sequence 1, Application US-0909348A1
Patent No. US0020042373A1
GENERAL INFORMATION:
APPLICANT: Bergmann, John
APPLICANT: Stierberg, Janet
APPLICANT: Crowther, Roger S.
APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Recurrent Application NUMBER: 3033-1003-001
CURRENT APPLICATION NUMBER: US-09/909-348-1
CURRENT FILING DATE: 2001-07-19
PRIORITY APPLICATION NUMBER: US-67/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0

QY

1 CBGDGGFPV 10
1 CBGDGGFPV 10
DB

;

RESULT 2
US-09-909-122-1
US-09-909-122-1
; sequence 1, Application US-0909122A1

Patent No. US20020128202A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jiping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 TITLE OF INVENTION: Peptide Derivatives
 FILE REFERENCE: 3033.1002-001
 CURRENT APPLICATION NUMBER: US/09/909,122
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-122-1

Query Match Score 59; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CEGDSGGPFY 10
 Db 1 CEGDSGGPFY 10

RESULT 3

US-10-050-692-1
 Sequence 1, Application US/10050692
 Publication No. US20020182205A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jiping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 TITLE OF INVENTION: PEPTIDE DERIVATIVES
 FILE REFERENCE: 3033.1002-004
 CURRENT APPLICATION NUMBER: US/10/050,692
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fragment of human prothrombin
 US-10-050-692-1

Query Match Score 59; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CEGDSGGPFY 10
 Db 1 CEGDSGGPFY 10

RESULT 4

US-10-050-688-1
 Sequence 1, Application US/10050688
 Publication No. US20020198154A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Stierberg, Janet
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
 TITLE OF INVENTION: Peptide fragment of thrombin
 FILE REFERENCE: 3033.1003-004
 CURRENT APPLICATION NUMBER: US/10/050,688
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,348
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,800
 PRIOR FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: peptide fragment of thrombin
 US-10-050-688-1

RESULT 5

US-09-909-348-2
 Sequence 2, Application US/09909348
 Parent No. US20042373A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Stierberg, Janet
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists Of The Non- Proteolytically Activated Thrombin Rec
 FILE REFERENCE: 3033.1003-001
 CURRENT APPLICATION NUMBER: US/09/909,348
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 60/219,800
 PRIOR FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of Thrombin
 NAME/KEY: VARIANT
 LOCATION: (1)...(10)
 OTHER INFORMATION: Xaa at position two is Glu or Gln
 OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
 US-09-909-348-2

Query Match Score 46; DB 9; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.83;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CEGDGGPFV 10
 Db 1 CGDGGPFV 10

RESULT 6
US-09-909-122-2
Sequence 2, Application US/09090122
Patent No. US20020128220A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
CROWHER, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jiping
APPLICANT: Redin, William R.
TITLE OF INVENTION: Simulation Of Bone Growth With Thrombin
FILE REFERENCE: 3033-1002-001
CURRENT APPLICATION NUMBER: US/09/909,122
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide fragment of Thrombin
NAME/KEY: VARIANT
LOCATION: (1) .. (10)
OTHER INFORMATION: Xaa at position two is Glu or Gln
OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-122-2

Query Match 78.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.83; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CEGDGGGPVY 10
Db 1 CXGDSGGPVY 10

FEATURE:
NAME/KEY: VARIANT
LOCATION: (9) .. (9)
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-2

Query Match 78.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.83; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CEGDGGGPVY 10
Db 1 CXGDSGGPVY 10

RESULT 7
US-10-050-692-2
Sequence 2, Application US/10050692
Publication No. US20020182205A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
CROWHER, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jiping
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
FILE REFERENCE: 3033-1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide fragment of thrombin
NAME/KEY: VARIANT
LOCATION: (2) .. (2)
OTHER INFORMATION: Xaa = Glu or Gln
FEATURE:
NAME/KEY: VARIANT
LOCATION: (9) .. (9)
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-2

Query Match 78.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.83; Indels 0; Gaps 0;

Qy 1 CEGDGGGPVY 10
Db 1 CXGDSGGPVY 10

RESULT 9
US-09-572-404B-605
Sequence 605, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary Peptide ligands from the human genome
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: Protpatent version 1.0

FEATURE:
NAME/KEY: VARIANT
LOCATION: (2) .. (2)
OTHER INFORMATION: Human fragment of prothrombin
FEATURE:
NAME/KEY: VARIANT
LOCATION: (2) .. (2)
OTHER INFORMATION: Xaa = Glu or Gln

SEQ ID NO 606
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens

OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence US-09-572-404B-606

FEATURE:
 OTHER INFORMATION: this patent.

Query Match Score 57.6%; Score 34; DB 10; Length 10;
 Best Local Similarity 71.4%; Pred. No. 63;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDGG 7
 Db 2 CKGEGG 8

RESULT 10
 US-09-572-404B-3584
 Sequence 3584, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human, Patent
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProtPatent version 1.0
 SEQ ID NO 3584
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens

FEATURE:
 OTHER INFORMATION: sequence located in PXR1 OR PEKS at 811-820 and may interact with Sequence US-09-572-404B-3584

Query Match Score 47.5%; Score 28; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GDSGG 7
 Db 6 GDSGG 10

RESULT 11
 US-09-572-404B-3784
 Sequence 3784, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human, Patent
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProtPatent version 1.0
 SEQ ID NO 3784
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens

FEATURE:
 OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with Sequence US-09-572-404B-3784

Query Match Score 45.8%; Score 27; DB 10; Length 10;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 863-8864/9741
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Other
 LOCATION: 8
 OTHER INFORMATION: Undefined
 SEQUENCE DESCRIPTION: SEQ ID NO: 55:
 US-09-871-957-55

Query Match 42.4%; Score 25; DB 9; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CEGDSGG 7
 Db 1 CMGDSLQ 7

RESULT 14
 US-09-572-404B-51
 Sequence 51, Application US/09572404B

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human Patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 51

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE: OTHER INFORMATION: sequence located in CBFA2 OR AML1 at 360-369 and may interact with

US-09-572-404B-51

OTHER INFORMATION: sequence 52 in this patent.

Qy 6 GGPFF 9

Db 7 GGPFF 10

Query Match 42.4%; Score 25; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGPFF 9

Db 7 GGPFF 10

RESULT 15
 US-09-572-404B-53
 Sequence 53, Application US/09572404B

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human Patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 53

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2004, 07:16:14 ; Search time 26.1905 Seconds

98.874 Million cell updates/sec

Title: US-09-909-348-1

Pefect score: 59

Sequence: 1 CEGDSCPFV 10

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

Published Applications AA.*

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3: /cgn2_6/ptodata/1/pubpa/us05_NEW_PUB..pep:*

4: /cgn2_6/ptodata/1/pubpa/us06_PUBCOMB..pep:*

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14: /cgn2_6/ptodata/1/pubpa/us10B_PUBCOMB..pep:*

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17: /cgn2_6/ptodata/1/pubpa/us60_NEW_PUB..pep:*

18: /cgn2_6/ptodata/1/pubpa/us60_PUBCOMB..pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	9 US-09-909-348-1	Sequence 1, Appli
2	59	100.0	10	9 US-09-909-122-1	Sequence 1, Appli
3	59	100.0	10	13 US-10-050-692-1	Sequence 1, Appli
4	59	100.0	10	13 US-10-050-688-1	Sequence 2, Appli
5	59	100.0	12	9 US-09-909-090-2	Sequence 2, Appli
6	59	100.0	12	13 US-10-050-611-2	Sequence 3, Appli
7	59	100.0	23	9 US-09-777-328-8	Sequence 3, Appli
8	59	100.0	23	9 US-09-904-090-3	Sequence 6, Appli
9	59	100.0	23	13 US-10-050-612-6	Sequence 6, Appli
10	59	100.0	23	13 US-10-050-611-3	Sequence 3, Appli
11	59	100.0	23	13 US-10-050-611-4	Sequence 4, Appli
12	59	100.0	23	13 US-10-050-688-5	Sequence 5, Appli
13	59	100.0	23	13 US-09-909-648-6	Sequence 6, Appli
14	59	100.0	25	9 US-09-909-348-5	Sequence 5, Appli
15	59	100.0	25	9 US-09-909-122-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-09-909-348-1
; Sequence 1, Application US/0909348
; Patent No. US2002042373A1
; GENERAL INFORMATION:
;   APPLICANT: Carnes, Darrell H.
;   APPLICANT: Crowther, Roger S.
;   APPLICANT: Bergmann, John
;   TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
;   TITLE OF INVENTION: Of The Use Of Thrombin Recombinant Proteolytically Activated Thrombin Recombinant Proteins
;   FILE REFERENCE: 3033_1003_001
;   CURRENT APPLICATION NUMBER: US-09-909-348-1
;   CURRENT FILING DATE: 2001-07-19
;   PRIOR APPLICATION NUMBER: US 60/219,800
;   PRIOR FILING DATE: 2000-07-20
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FASTSEQ for Windows Version 4.0
;   SEQ ID NO: 1
;   LENGTH: 10
;   TYPE: PRT
;   FEATURES:
;   ORGANISM: Artificial Sequence
;   OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-1
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Query Match          100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Prd. 0.0076; Indels 0; Mismatches 0;
Matches 10; Conservative 0;
Qy 1 CEGDSCPFV 10
Db 1 CEGDSCPFV 10
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RESULT 2
US-09-909-122-1
; Sequence 1, Application US/09093122
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Patent No. US20020128202A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: Stimulation of Bone Growth With Thrombin
 FILE REFERENCE: 3033.1000-001
 CURRENT APPLICATION NUMBER: US/09/909.122
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 5
 SEQ ID NO: 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide Fragment of Thrombin
 US-09-909-122-1

Query Match 100.0%; Score 59; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDGGPFV 10
 Db 1 CEGDGGPFV 10

RESULT 3
 Sequence 1, Application US/10050692
 Publication No. US20020182205A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 PEPTIDE DERIVATIVES
 FILE REFERENCE: 3033.1002-004
 CURRENT APPLICATION NUMBER: US/10/050,692
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 6
 SEQ ID NO: 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: fragment of human prothrombin
 US-10-050-692-1

Query Match 100.0%; Score 59; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDGGPFV 10
 Db 1 CEGDGGPFV 10

Sequence 1, Application US/10050688
 Publication No. US20020198154A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Stierberg, Jane
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
 FILE REFERENCE: 3033.1003-004
 CURRENT APPLICATION NUMBER: US/10/050,688
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,348
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,800
 PRIOR FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of thrombin
 US-10-050-688-1

Query Match 100.0%; Score 59; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDGGPFV 10
 Db 1 CEGDGGPFV 10

RESULT 5
 US-09-904-090-2
 Sequence 2, Application US/09904090
 Patent No. US20020161852A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 PEPTIDES
 FILE REFERENCE: 3033.1000-001
 CURRENT APPLICATION NUMBER: US/09/904,090
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: US 60/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Polypeptide, fragment of thrombin
 US-09-904-090-2

Query Match 100.0%; Score 59; DB 9; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0091;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDGGPFV 10
 Db 3 CEGDGGPFV 12

RESULT 6
 US-10-050-611-2
 Sequence 2, Application US/10050611
 Publication No. US20020187933A1
 GENERAL INFORMATION:

RESULT 4
 US-10-050-688-1

APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 PEPTIDES
 FILE REFERENCE: 3033.1000-008
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/904,090
 PRIOR FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 60/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: human fragment of thrombin
 US-10-050-611-2

Query Match 100.0%; Score 59; DB 9; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0091; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 CEGDGGPPV 10
 Db 3 ||||| |||||
 14 CEGDGGPPV 12

RESULT 7
 US-09-777-328-8
 Sequence 8, Application US/09777328
 Patent No. US20032314A1
 GENERAL INFORMATION:
 APPLICANT: CAREY, DARREL H.
 TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
 FILE REFERENCE: CHPB:002
 CURRENT APPLICATION NUMBER: US/09/777,328
 CURRENT FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: 08/330,594
 PRIOR FILING DATE: 1994-10-28
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 8
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-777-328-8

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 Best Local Similarity 100.0%; Pred. No. 0.017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 CEGDGGPPV 10
 Db 14 ||||| |||||
 14 CEGDGGPPV 23

RESULT 8
 US-09-904-090-3
 Sequence 3, Application US/09904090
 Patent No. US200201855A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 PEPTIDES
 FILE REFERENCE: 3033.1000-001
 CURRENT APPLICATION NUMBER: US/09/904,090
 CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US 60/217,583
 PRIORITY: 3033.1000-008
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Polypeptide, fragment of thrombin
 US-09-904-090-3

Query Match 100.0%; Score 59; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 CEGDGGPPV 10
 Db 14 ||||| |||||
 14 CEGDGGPPV 23

RESULT 9
 US-10-050-6192-6
 Sequence 6, Application US/10050692
 Publication No. US000182205A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jiping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 FILE REFERENCE: 3033.1002-004
 CURRENT APPLICATION NUMBER: US/10/050,692
 CURRENT FILING DATE: 2000-01-16
 PRIOR APPLICATION NUMBER: 09/909,122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,300
 PRIOR FILING DATE: 2000-07-19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: c-terminal amidated fragment of human thrombin
 FEATURE:
 NAME/KEY: AMIDATION
 LOCATION: (23) .. (23)
 OTHER INFORMATION: valine is amidated as CONH2

US-10-050-6192-6

Query Match 100.0%; Score 59; DB 13; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 CEGDGGPPV 10
 Db 14 ||||| |||||
 14 CEGDGGPPV 23

RESULT 10
 US-10-050-611-3
 Sequence 3, Application US/10050611
 Publication No. US20020187933A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 PEPTIDES
 FILE REFERENCE: 3033.1000-008
 CURRENT APPLICATION NUMBER: US/10/050,611

RESULT 11
US-10-050-611-4
/ Sequence 4, Application US/10050611
/ PUBLICATION NO. US2002018793A1
/ GENERAL INFORMATION:
/ APPLICANT: Carney, Darrell H.
/ TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
/ TITLE OF INVENTION: PEPTIDES
/ FILE REFERENCE: 3:033 1000-008
/ CURRENT APPLICATION NUMBER: US/10/050,611
/ CURRENT FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 09/904,090
/ PRIOR FILING DATE: 2001-07-12
/ PRIOR APPLICATION NUMBER: 60/217,583
/ PRIOR FILING DATE: 2000-07-12
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 23
/ TYPE: PRT
/ FEATURE:
/ OTHER INFORMATION: human fragment of thrombin
US-10-050-611-3
Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CEGDGGPPV 10
Db 14 CEGDGGPPV 23

RESULT 12
US-10-050-688-5
/ Sequence 5, Application US/10050688
/ Publication No. US20020198154A1
/ GENERAL INFORMATION:
/ APPLICANT: Carney, Darrell H.
/ APPLICANT: Crowther, Roger S.
/ APPLICANT: Stierberg, Janet
/ APPLICANT: Bergmann, John
/ TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
/ FILE REFERENCE: 3:033 1003-004
/ CURRENT APPLICATION NUMBER: US/10/050,688
/ CURRENT FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 09/909,348
/ PRIOR FILING DATE: 2001-07-19
/ PRIOR APPLICATION NUMBER: 60/219,800
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Fast-SEQ for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 23
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide fragment of thrombin
/ NAME/KEY: AMIDATION
/ LOCATION: 23
/ OTHER INFORMATION: valine is amidated as CONH2
US-10-050-611-4
Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CEGDGGPPV 10
Db 14 CEGDGGPPV 23

RESULT 13
US-10-050-688-6
/ Sequence 6, Application US/10050688
/ Publication No. US20020198154A1
/ GENERAL INFORMATION:
/ APPLICANT: Carney, Darrell H.
/ APPLICANT: Crowther, Roger S.
/ APPLICANT: Stierberg, Janet
/ APPLICANT: Bergmann, John
/ TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
/ FILE REFERENCE: 3:033 1003-004
/ CURRENT APPLICATION NUMBER: US/10/050,688
/ CURRENT FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 09/909,348
/ PRIOR FILING DATE: 2001-07-19
/ PRIOR APPLICATION NUMBER: 60/219,800
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Fast-SEQ for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 23
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide fragment of thrombin
/ NAME/KEY: AMIDATION
/ LOCATION: (23) .(23)
/ OTHER INFORMATION: CONH2
US-10-050-688-6
Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CEGDGGPPV 10
Db 14 CEGDGGPPV 23

RESULT 14
US-03-909-348-5
/ Sequence 5, Application US/09909348
/ Publication No. US20020198154A1
/ GENERAL INFORMATION:
/ APPLICANT: Carney, Darrell H.
/ APPLICANT: Crowther, Roger S.
/ APPLICANT: Stierberg, Janet
/ APPLICANT: Bergmann, John
/ TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
/ TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN

GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Protectolytically Activated Thrombin Receptor
; FILE REFERENCE: 3033-1002-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin

US-09-909-348-5

Query Match	100.0%	Score 59;	DB 9;	Length 25;	
Best Local Similarity	100.0%	Pred. No. 0.018;			
Matches	10;	Mismatches	0;	Indels	0;
Qy	1	CEGDGGPFV	10		
Db	16	CEGDGGPFV	25		

RESULT 15
US-09-909-122-5
Sequence 5 Application US/09909122
Patent No. US20030128502A1
GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiriping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033-1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin

US-09-909-122-5

Query Match	100.0%	Score 59;	DB 9;	Length 25;	
Best Local Similarity	100.0%	Pred. No. 0.018;			
Matches	10;	Mismatches	0;	Indels	0;
Qy	1	CEGDGGPFV	10		
Db	16	CEGDGGPFV	25		

Search completed: March 18, 2004, 07:24:51
Job time : 27.1905 secs

Gencore version 5.1.6
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 run on: March 18, 2004 ; Search time 33.5 Seconds
 (without alignments)
 77.300 Million cell updates/sec

title: US-09-909-348-2
 perfect score: 50
 sequence: 1 CXGDSGPXV 10
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 1049977 seqs, 258955319 residues
 total number of hits satisfying chosen parameters: 32147

minimum DB seq length: 10
 maximum DB seq length: 10

post-processing: Maximum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Published Applications All:
 database : Sequence 2033, AP
 Sequence 2091, AP
 Sequence 2093, AP
 Sequence 2095, AP
 Sequence 196, APP
 Sequence 204, APP
 Sequence 206, APP
 Sequence 9, APP
 Sequence 4, APP
 Sequence 27, APP
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 Sequence 496, APP
 Sequence 25, APP
 Sequence 54, APP
 Sequence 114, APP
 Sequence 176, APP
 Sequence 342, APP
 Sequence 344, APP
 Sequence 1306, APP
 Sequence 2218, APP
 Sequence 2332, APP
 Sequence 2668, APP
 Sequence 2798, APP
 Sequence 3152, APP
 Sequence 3354, APP
 Sequence 3356, APP

ALIGNMENTS

RESULT 1
US-09-909-348-1

/ Sequence 1, Application US/09909348
 / Patent No. US20020042373A1
 / GENERAL INFORMATION:
 / APPLICANT: Carney, Darrell H.
 / CROWDER, Roger S.
 / APPLICANT: Stiernberg, Janet
 / APPLICANT: Bergmann, John
 / TITLE OF INVENTION: Simulation Of Cartilage Growth With Agonists
 / TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin
 / FILE REFERENCE: 3033.1003-001
 / CURRENT APPLICATION NUMBER: US/09/909,348
 / CURRENT FILING DATE: 2001-07-19
 / PRIOR APPLICATION NUMBER: US 60/219,800
 / PRIOR FILING DATE: 2000-07-20
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 1
 LENGTH: 10
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-348-1

Query 1 CGXGDSGGPXY 10
 Best Local Similarity 92.0%; Score 46; DB 9; Length 10;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CGXGDSGGPXY 10
 Db 1 CGEGDSGGPFPV 10

RESULT 2
US-09-909-348-2

/ Sequence 2, Application US/09909348
 / Patent No. US20020042373A1
 / GENERAL INFORMATION:
 / APPLICANT: Carney, Darrell H.
 / CROWDER, Roger S.
 / APPLICANT: Stiernberg, Janet
 / APPLICANT: Bergmann, John
 / TITLE OF INVENTION: Simulation Of Cartilage Growth With Agonists
 / TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin
 / FILE REFERENCE: 3033.1003-001
 / CURRENT APPLICATION NUMBER: US/09/909,348
 / CURRENT FILING DATE: 2001-07-19
 / PRIOR APPLICATION NUMBER: US 60/219,800
 / PRIOR FILING DATE: 2000-07-20
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 1
 LENGTH: 10
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-348-1

Query 1 CGXGDSGGPXY 10
 Best Local Similarity 80.0%; Pred. No. 0.37;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SUMMARIES

result	No.	Score	Query	Match	Length	DB	ID
1	46	92.0		10	9	US-09-909-348-1	
2	46	92.0		10	9	US-09-909-348-2	
3	46	92.0		10	9	US-09-909-1122-1	
4	46	92.0		10	9	US-09-909-1122-2	
5	46	92.0		13	13	US-10-050-692-1	
6	46	92.0		10	13	US-10-050-692-2	
7	46	92.0		10	13	US-10-050-688-1	
8	46	92.0		10	13	US-10-050-688-2	
9	32	64.0		10	10	US-09-572-404B-606	
10	28	56.0		10	10	US-09-572-404B-3584	
11	27	54.0		10	10	US-09-572-404B-3784	
12	27	54.0		10	10	US-09-572-404B-3785	
13	26	52.0		10	9	US-09-879-957-55	
14	25	50.0		10	10	US-09-572-404B-174	
15	25	50.0		10	10	US-09-572-404B-2027	

Patent No. US20020042373A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Stieremberg, Janet
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
 TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin
 FILE REFERENCE: 3033-1002-001
 CURRENT APPLICATION NUMBER: US/09/909,348
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 60/219,800
 PRIOR FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of Thrombin
 NAME/KEY: VARIANT
 LOCATION: (1) ... (10)
 OTHER INFORMATION: Xaa at position two is Glu or Gln
 OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
 US-09-909-348-2

Query Match	92.0%	Score 46;	DB 9;	Length 10;	
Best Local Similarity	100.0%	Pred. No 0.37;	Indels 0;	Gaps 0;	
Matches	10;	Conservative 0;	Mismatches 0;		

Qy 1 CXGDSGGPXY 10
 Db 1 CXGDSGGPXY 10

RESULT 3
 US-09-909-122-1
 / Sequence 1, Application US/09909122
 / Patent No. US20020128202A1
 / GENERAL INFORMATION:
 / APPLICANT: Carney, Darrell H.
 / APPLICANT: Crowther, Roger S.
 / APPLICANT: Simmons, David J.
 / APPLICANT: Yang, Jinping
 / APPLICANT: Redin, William R.
 / TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 / FILE REFERENCE: 3033-1002-001
 / CURRENT APPLICATION NUMBER: US/09/909,122
 / CURRENT FILING DATE: 2001-07-19
 / PRIOR APPLICATION NUMBER: US 60/219,300
 / PRIOR FILING DATE: 2000-07-19
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 1
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-122-1

Query Match	92.0%	Score 46;	DB 9;	Length 10;	
Best Local Similarity	80.0%	Pred. No 0.37;	Indels 2;	Gaps 0;	
Matches	8;	Conservative 0;	Mismatches 0;		

Qy 1 CXGDSGGPXY 10
 Db 1 CEGDGGFPV 10

RESULT 4
 US-09-909-122-2
 / Sequence 2, Application US/09909122
 / Patent No. US20020128202A1
 / GENERAL INFORMATION:
 / APPLICANT: Carney, Darrell H.
 / APPLICANT: Crowther, Roger S.
 / APPLICANT: Simmons, David J.
 / APPLICANT: Yang, Jinping
 / APPLICANT: Redin, William R.
 / TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 / FILE REFERENCE: 3033-1002-001
 / CURRENT APPLICATION NUMBER: US/09/909,122
 / CURRENT FILING DATE: 2001-07-19
 / PRIOR APPLICATION NUMBER: US 60/219,300
 / PRIOR FILING DATE: 2000-07-19
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 2
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Peptide Derivatives
 US-09-909-122-2

Query Match	92.0%	Score 46;	DB 13;	Length 10;	
Best Local Similarity	80.0%	Pred. No 0.37;	Indels 2;	Gaps 0;	
Matches	8;	Conservative 0;	Mismatches 0;		

Qy 1 CXGDSGGPXY 10
 Db 1 CXGDSGGPXY 10

RESULT 12
US-09-572-404B-3785
; Sequence 3785, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd.
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO: 3785
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with US-09-572-404B-3785 in this patent.

Query Match 64.0%; Score 32; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGDGGG 7
Db 2 CKGESEGG 8

RESULT 10
US-09-572-404B-3584
; Sequence 3584, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd.
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO: 3584
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PKR1 OR PEX5 at 811-820 and may interact with US-09-572-404B-3584 in this patent.

Query Match 56.0%; Score 28; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GDSGG 7
Db 6 GDSGG 10

RESULT 11
US-09-572-404B-3784
; Sequence 3784, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd.
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO: 3784
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with US-09-572-404B-3784 in this patent.

Query Match 54.0%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDGGGP 8
Db 3 GASGGP 8

RESULT 13
US-09-879-957-55
; Sequence 55, Application US/09879957
; Patent No. US2002034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US2002034755A1
; KAY, Brian K.
; POWLES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879, 957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIORITY DATA:
; APPLICATION NUMBER: US 08/630, 915
; FILING DATE: 03-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 FEATURE: NAME/KEY: Other
 LOCATION: 8 OTHER INFORMATION: Undefined
 SEQUENCE DESCRIPTION: SEQ ID NO: 55:
 US-09-879-957-55

Query Match 52.0%; Score 26; DB 9; Length 10;
 Best Local Similarity 71.4%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CXGDDGG 7
 Db 1 CMGDSLIG 7

RESULT 14
 US-09-572-404B-174
 Sequence 174, Application US/0972404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human Patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProtPatent version 1.0
 SEQ ID NO 174
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:
 OTHER INFORMATION: sequence located in EPHB4 OR HTK at 974-983 and may interact with
 OTHER INFORMATION: Sequence 173 in this patent.

US-09-572-404B-174
 Sequence 174, Application US/0972404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human Patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProtPatent version 1.0
 SEQ ID NO 2027
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:

OTHER INFORMATION: sequence located in CNTFR at 340-349 and may interact with Sequence
 OTHER INFORMATION: in this patent.
 US-09-572-404B-2027
 Query Match 50.0%; Score 25; DB 10; Length 10;
 Best Local Similarity 66.7%; Pred. No. 9.9e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 GDGGGP 8
 Db 2 GSGGGP 7
 Search completed: March 18, 2004, 07:26:10
 Job time : 33.5 secs

Query Match 50.0%; Score 25; DB 10; Length 10;
 Best Local Similarity 66.7%; Pred. No. 9.9e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 GDGGGP 8
 Db 5 GGTGGP 10

RESULT 15
 US-09-572-404B-2027
 Sequence 2027, Application US/0972404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human Patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProtPatent version 1.0
 SEQ ID NO 2027
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:


```

TITLE OF INVENTION: A Protease and an Aminopeptidase Associated with Development of BPH
; TITLE OF INVENTION: Prostatic Hyperplasia (BPH)
; FILE REFERENCE: 2024-451
; CURRENT APPLICATION NUMBER: US/09/860,739
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-739-1

RESULT 3
US-10-128-966-7
; Sequence 7, Application US/10128966
; Publication No. US20030113743A1
; GENERAL INFORMATION:
; APPLICANT: Slawir, K. M.
; APPLICANT: Tindall, D. J.
; APPLICANT: Young, C.Y.F.
; APPLICANT: Saedi, M.S.
; APPLICANT: Kumar, A.
; APPLICANT: Wolfert, R.L.
; APPLICANT: Rittichier, H.G.
; TITLE OF INVENTION: Method for detection of micrometastatic
; TITLE OF INVENTION: Prostate cancer.
; FILE REFERENCE: 675_001USI
; CURRENT APPLICATION NUMBER: US/10/128,966
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US/08/843,076D
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 08/759,354
; PRIOR FILING DATE: 1998-11-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-966-7

Query Match 94.0%; Score 47; DB 14; Length 237;
Best Local Similarity 80.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
GENERAL INFORMATION:
Qy 1 CXGDSGGPXY 10
Db 185 CSGDSGGPLV 194

RESULT 4
US-10-14-671-21
; Sequence 21, Application US/10148671
; Publication No. US20030186419A1
; GENERAL INFORMATION:
; APPLICANT: Jersennus, Jens Christian
; APPLICANT: Thiel, Steffen
; TITLE OF INVENTION: MASSP-3, A complement-fixing enzyme, and uses for it
; FILE REFERENCE: 10/148,671
; CURRENT APPLICATION NUMBER: US/10/148,671
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: PCT/DK00/00659
; PRIOR FILING DATE: 2000-11-30

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NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 21
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens (fig. 10, humASP-1)
US-10-148-671-21

Query Match Score 94.0%; DB 14; Length 252;
Best Local Similarity 80.0%; Pred. No. 4,9;
Matches 8; Conservative 0; Mismatches 2; Indels 0

Qy      1 CXGDSGGGXXV 10
Db      195 CAGDSGGGPWV 204

RESULT 5
US-09-796-294-10
Sequence 10, Application US/09796294
Patent No. US20020037581A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Extracellular Serine Protease
FILE REFERENCE: D6120CIP3
CURRENT APPLICATION NUMBER: US/09/796,294
PRIORITY APPLICATION NUMBER: US/09/618,259
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 72
SEQ ID NO: 10
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Amino acid sequence of Prostate Specific
OTHER INFORMATION: (hPSA); accession no. P07288
US-09-796-294-10

Query Match Score 94.0%; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5,1;
Matches 8; Conservative 0; Mismatches 2; Indels 0

Qy      1 CXGDSGGGPXV 10
Db      209 CSGDSSGGPPLY 218

RESULT 6
US-09-822-827-946
Sequence 946, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianghun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534.C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SEQ ID NO: 946
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-946

Query Match Score 94.0%; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5,1;
Matches 8; Conservative 0; Mismatches 2; Indels 0

Qy      1 CXGDSGGPXY 10

```

Db 209 ||||| CSGDGGPVL 218

RESULT 7
US-09-896-6
Sequence 6; Application US/09963896
Patent No. US2002010585A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti.
Coley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/963,896
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/397,558
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 130989
SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

US-09-963-896-6

Query Match 94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGPXV 10
Db 209 CSGDGGPVL 218

RESULT 8
US-09-907-402-1
Sequence 1; Application US/09907402
Patent No. US20020137668A1
GENERAL INFORMATION:
APPLICANT: Holiday, John W.
APPLICANT: Portier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0343 43170-261379
CURRENT APPLICATION NUMBER: US/09/907,402
CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-307-402-1

Query Match 94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGPXV 10
Db 209 CSGDGGPVL 218

RESULT 9
US-09-895-793-946
Sequence 946; Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiaochun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocke, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Ritter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghon, Patricia L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121_534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO: 946
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-793-946

Query Match 94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGPXV 10
Db 209 CSGDGGPVL 218

RESULT 10

US-10-131-241-62
Sequence 62 Application US/10131241
 GENERAL INFORMATION:
 Publication No. US20030012792A1
 APPLICANT: Holdaway, John W.
 PRIORITY: Portier, Anne H.
 TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
 FILE REFERENCE: 05213-0344 431170-271555
 CURRENT APPLICATION NUMBER: US/10131,241
 PRIOR APPLICATION NUMBER: US 09/413,049
 PRIOR FILING DATE: 1999-10-06
 PRIOR APPLICATION NUMBER: US 60/086,586
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 62
 LENGTH: 261
 TYPE: PRT
 ORGANISM: Homo sapiens
 SEQ-10-131-241-62

Query Match 94.0%; Score 47; DB 14; Length 261;
 Best Local Similarity 80.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;

US-10-131-241-62

Qy 1 CXGDSGGPXY 10
 Db 209 CSGDGGPPLY 218

RESULT 11
 US-10-461-787-10
Sequence 10, Application US/10461787
 Publication No. US200301990-0A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 PRIORITY: Underwood, Lowell J.
 TITLE OF INVENTION: US20030199010A1 Extracellular Serine Protease
 FILE REFERENCE: D6020CIP2
 CURRENT APPLICATION NUMBER: US/10/461,787
 PRIOR FILING DATE: 2003-06-13
 PRIOR APPLICATION NUMBER: US/09/618,259
 PRIOR FILING DATE: 2000-07-18
 PRIOR APPLICATION NUMBER: US 09/127,444
 PRIOR FILING DATE: 1998-08-21
 NUMBER OF SEQ ID NOS: 72
 SEQ ID NO: 10
 LENGTH: 261
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of Prostate Specific Antigen
 SEQ-10-461-787-10

Query Match 94.0%; Score 47; DB 14; Length 261;
 Best Local Similarity 80.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;

US-10-461-787-10

Qy 1 CXGDSGGPXY 10
 Db 209 CSGDGGPPLY 218

RESULT 12
 US-10-298-965-18
Sequence 18, Application US/10298965
 Publication No. US20030207808A1
 GENERAL INFORMATION:

RESULT 14
US-10-341-434-34
Sequence 34, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
US-10-341-434-34

Query Match 94.0%; Score 47; DB 15; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 209 CSGDSSGPPLY 218

RESULT 15
US-10-341-434-41
Sequence 41, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
US-10-341-434-41

Query Match 94.0%; Score 47; DB 15; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CXGDSGGPXY 10
Db 209 CSGDSSGPPLY 218

Search completed: March 18, 2004, 07:24:51
Job time : 26.1905 secs

Copyright GenCore version 5.1.6
(C) 1993 - 2004 Compugen Ltd.

OM: Protein - protein search, using SW model

Run on: March 18, 2004, 07:17:54 ; Search time 39 Seconds

(without alignments)
26.560 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21 RGDA 4

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 25855339 residues

Total number of hits satisfying chosen parameters: 5333

Minimum DB seq length: 4

Maximum DB seq length: 4

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	21	100.0	4	9 US-09-904-190-1	Sequence 1, Appli
3	21	100.0	4	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4	10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4	13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4	13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4	13 US-10-050-688-3	Sequence 3, Appli
8	21	100.0	4	14 US-10-200-879-23	Sequence 23, Appli
9	18	85.7	4	9 US-09-823-144-6	Sequence 6, Appli
10	18	85.7	4	9 US-09-010-714-9	Sequence 9, Appli
11	18	85.7	4	9 US-09-925-115-21	Sequence 21, Appli
12	18	85.7	4	9 US-09-935-168-1	Sequence 1, Appli
13	18	85.7	4	9 US-09-942-117-5	Sequence 5, Appli
14	18	85.7	4	10 US-09-911-569-22	Sequence 22, Appli
15	18	85.7	4	11 US-09-990-050-1	Sequence 23, Appli

Sequence 10, Appli

SUMMARIES

ALIGNMENTS					
US-09-909-348-3	Sequence 3, Application US/09090348	; Patent No. US0020042373A1	; GENERAL INFORMATION:	; APPLICANT: Carney, Darrell H.	
				; APPLICANT: Crowder, Roger S.	
				; APPLICANT: Stierberg, Janet	
				; APPLICANT: Bergmann, John	
				; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists	
				; FILE REFERENCE: 3033.1003-001	
				; CURRENT APPLICATION NUMBER: US/09/909-348	
				; CURRENT FILING DATE: 2001-07-19	
				; PRIORITY NUMBER: US 60/219,800	
				; PRIORITY FILING DATE: 2000-07-20	
				; NUMBER OF SEQ ID NOS: 5	
				; SOFTWARE: FastSEQ for Windows Version 4.0	
				; SEQ ID NO: 3	
				; LENGTH: 4	
				; TYPE: PRT	
				; ORGANISM: Artificial Sequence	
				; FEATURE:	
				; OTHER INFORMATION: Peptide fragment of Thrombin	
				; US-09-909-348-3	

RESULT 2

US-09-304-050-1

; Sequence 1, Application US/0904050

Patent No. US20020061852A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED PEPTIDES
 FILE REFERENCE: 3033-1000-001
 CURRENT APPLICATION NUMBER: US/09/904,090
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: US 60/217,583
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Polypeptide, fragment of thrombin

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
 Db 1 RGDA 4

RESULT 3
 US-09-909-122-3
 / Sequence 3, Application US/090909122
 / Patent No. US200200128202A1
 / GENERAL INFORMATION:
 / APPLICANT: Carney, Darrell H.
 / CROWDER, Roger S.
 / SIMMONS, David J.
 / APPLICANT: Yang, Jinping
 / APPLICANT: Redin, William R.
 / TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 / TITLE OF INVENTION: Peptide Derivatives
 / FILE REFERENCE: 3033-1002-001
 / CURRENT APPLICATION NUMBER: US/09/909,122
 / CURRENT FILING DATE: 2001-07-19
 / PRIOR APPLICATION NUMBER: US 60/219,300
 / PRIOR FILING DATE: 2000-07-19
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 3
 / LENGTH: 4
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE: OTHER INFORMATION: Peptide Fragment of Thrombin

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
 Db 1 RGDA 4

RESULT 4
 US-09-911-569-23
 / Sequence 23, Application US/090911569
 / Publication No. US20030069173A1
 / GENERAL INFORMATION:
 / APPLICANT: HAWLEY-NELSON, PAMELA
 / LAN, JIANGING
 / SHIH, POJEN

JESSE, JOEL A.
 SCHIFFERLI, KEVIN P.
 GEBEYEHU, GUILIAH
 TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GREENBEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/911,569
 FILING DATE: 23-JUL-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/039,780
 FILING DATE: 16-MAR-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: SULLIVAN, SALLY A.
 REGISTRATION NUMBER: 32,064
 REFERENCE/DOCKET NUMBER: 32-95D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303)499-8080
 TELEFAX: (303)499-8089
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-911-569-23
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 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGDA 4
 Db 1 RGDA 4

RESULT 5
 US-10-010-692-3
 / Sequence 3, Application US/10050692
 / Publication No. US2002082203A1
 / GENERAL INFORMATION:
 / APPLICANT: Carney, Darrell H.
 / CROWDER, Roger S.
 / SIMMONS, David J.
 / APPLICANT: Yang, Jinping
 / APPLICANT: Redin, William R.
 / TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 / FILE REFERENCE: 3033-1002-004
 / CURRENT APPLICATION NUMBER: US/10/050,692
 / CURRENT FILING DATE: 2002-1-16
 / PRIOR APPLICATION NUMBER: 09/905,122
 / PRIOR FILING DATE: 2001-07-19
 / PRIOR APPLICATION NUMBER: 60/219,300
 / PRIOR FILING DATE: 2000-07-19
 / NUMBER OF SEQ ID NOS: 6
 / SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO: 3
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: fragment of human prothrombin
 US-10-050-692-3

Query Match	100.0%	Score 21;	DB 13;	Length 4;
Best Local Similarity	100.0%	Pred. No.	9.5e+05;	
Matches	4;	Conservative	0;	Mismatches 0;
Qy	1 RGDA 4			Indels 0;
Db	1 RGDA 4			Gaps 0;

RESULT 6
 US-10-050-611-1
 Sequence 1, Application US/10050611
 Publication No. US2002018933A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 PEPTIDES
 FILE REFERENCE: 3033.1000-008
 CURRENT APPLICATION NUMBER: US/10/050,611
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/904,090
 PRIOR FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 60/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NO: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: human fragment of thrombin
 US-10-050-611-1

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Best Local Similarity	100.0%	Pred. No.	9.5e+05;	
Matches	4;	Conservative	0;	Mismatches 0;
Qy	1 RGDA 4			Indels 0;
Db	1 RGDA 4			Gaps 0;

RESULT 7
 US-10-050-688-3
 Sequence 3, Application US/10050688
 Publication No. US2002019815A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Stierberg, Janet
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
 AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
 CURRENT APPLICATION NUMBER: US/10/050,688
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 3033.1003-004
 FILE REFERENCE: 3033.1003-004
 PRIOR FILING DATE: 2001-07-19
 NUMBER OF SEQ ID NO: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3

LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: peptide fragment of thrombin
 US-10-050-688-3

Query Match	100.0%	Score 21;	DB 13;	Length 4;
Best Local Similarity	100.0%	Pred. No.	9.5e+05;	
Matches	4;	Conservative	0;	Mismatches 0;
Qy	1 RGDA 4			Indels 0;
Db	1 RGDA 4			Gaps 0;

RESULT 8
 US-10-200-879-23
 Sequence 23, Application US/10200879
 Publication No. US2003014423A1
 GENERAL INFORMATION:
 APPLICANT: Hawley-Nelson, Pamela
 Lan, Jianping
 Shih, Pojen
 Jesse, Joel A.
 Schifferli, Guiliat P.
 GEBEYEHU, GUILLIAT P.
 TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: GREENLEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/200,879
 FILING DATE: 23-JUL-2002
 CLASSIFICATION: Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/9/911,569
 FILING DATE: 23-JUL-2001
 APPLICATION NUMBER: US/9/939,780
 FILING DATE: 16-MAR-1998
 APPLICATION NUMBER: US/98/818,200
 FILING DATE: 14-MAR-1997
 APPLICATION NUMBER: US/98/658,130
 FILING DATE: 04-JUN-1996
 APPLICATION NUMBER: US/9/939,780
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Sullivan, Sally A.
 REGISTRATION NUMBER: 32,064
 REFERENCE DOCKET NUMBER: 32-95E
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303)499-8080
 TELEFAX: (303)499-8089
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:


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; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-5

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Best Local Similarity 75.0%;  Pred. No. 9.5e+05;
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Qy      1  RGDA 4
Db      1  RGDS 4

RESULT 14
US-09-911-569-22
Sequence 22. Application US/09911569
Publication No. US20030069173A1
GENERAL INFORMATION:
APPLICANT: HAN, JIANGQING
SHIH, POEON
JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
GEBUYEHU, GUILILAT

TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5170 MANHATTAN CIRCLE, SUITE 201
CITY: BOULDER
STATE: CO
COUNTRY: US
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/911-569
FILING DATE: 23-Jul-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE DOCKET NUMBER: 32-95D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8059
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: Linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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GenCore version 5.1.6
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Run on: March 18, 2004, 07:16:14 ; Search time 10.4762 Seconds

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4 10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 673, App
14	21	100.0	7 9 US-09-989-789-674	Sequence 674, App
15	21	100.0	7 9 US-09-989-789-675	Sequence 675, App

SUMMARY

Result No.	Score	Query Match Length	DB ID	Description
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2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
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5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 673, App
14	21	100.0	7 9 US-09-989-789-674	Sequence 674, App
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SUMMARY

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4 9 US-09-909-348-3	Sequence 3, Appli
2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4 10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 673, App
14	21	100.0	7 9 US-09-989-789-674	Sequence 674, App
15	21	100.0	7 9 US-09-989-789-675	Sequence 675, App

SUMMARY

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4 9 US-09-909-348-3	Sequence 3, Appli
2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4 10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 673, App
14	21	100.0	7 9 US-09-989-789-674	Sequence 674, App
15	21	100.0	7 9 US-09-989-789-675	Sequence 675, App

SUMMARY

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4 9 US-09-909-348-3	Sequence 3, Appli
2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4 10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 673, App
14	21	100.0	7 9 US-09-989-789-674	Sequence 674, App
15	21	100.0	7 9 US-09-989-789-675	Sequence 675, App

SUMMARY

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4 9 US-09-909-348-3	Sequence 3, Appli
2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4 10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 673, App
14	21	100.0	7 9 US-09-989-789-674	Sequence 674, App
15	21	100.0	7 9 US-09-989-789-675	Sequence 675, App

SUMMARY

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4 9 US-09-909-348-3	Sequence 3, Appli
2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4 10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 673, App
14	21	100.0	7 9 US-09-989-789-674	Sequence 674, App
15	21	100.0	7 9 US-09-989-789-675	Sequence 675, App

SUMMARY

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4 9 US-09-909-348-3	Sequence 3, Appli
2	21	100.0	4 9 US-09-904-00-1	Sequence 1, Appli
3	21	100.0	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4 10 US-09-911-169-23	Sequence 23, Appli
5	21	100.0	4 13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4 13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4 13 US-10-050-88-3	Sequence 3, Appli
8	21	100.0	4 14 US-10-200-879-23	Sequence 23, Appli
9	21	100.0	7 9 US-09-989-789-289	Sequence 289, App
10	21	100.0	7 9 US-09-989-789-670	Sequence 670, App
11	21	100.0	7 9 US-09-989-789-671	Sequence 671, App
12	21	100.0	7 9 US-09-989-789-672	Sequence 672, App
13	21	100.0	7 9 US-09-989-789-673	Sequence 6

Patent No. US20020061852A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 FILE REFERENCE: 3033-1000-001
 CURRENT APPLICATION NUMBER: US/09/904,050
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: US 67/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Polypeptide, fragment of thrombin
 US-09-904-090-1

Qy	1	RGDA	4	Score 21; DB 9; Length 4;
Db	1	RGDA	4	Best Local Similarity 100.0%; Pred. No. 9.5e+05; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-09-909-122-3
 Sequence 3, Application US/0909122
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 CROWTHER, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 FILE REFERENCE: 3033-1002-001
 CURRENT APPLICATION NUMBER: US/09/909,122
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 67/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-122-3

Qy	1	RGDA	4	Score 21; DB 9; Length 4;
Db	1	RGDA	4	Best Local Similarity 100.0%; Pred. No. 9.5e+05; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-09-911-569-23
 Sequence 23, Application US/09911569
 Publication No. US20030069173A1
 GENERAL INFORMATION:
 APPLICANT: HAWLEY-NELSON, PAMELA LAN, JIAQING SHI, POJEN

JESSE, JOEL A.
 SCHIFFERLI, KEVIN P.
 GEBEYEHU, GUILFAT
 TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GREENLEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentRelease #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/911,569
 FILING DATE: 23-JUL-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/039,780
 FILING DATE: 16-MAR-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: SULLIVAN, SALLY A.
 REGISTRATION NUMBER: 32,064
 REGISTRATION/DOCKET NUMBER: 32-95D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303)499-8080
 TELEFAX: (303)499-8089
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDBNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 SEQ ID NO: 23:
 US-09-911-569-23
 Query Match Score 21; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RGDA 4
 Db 1 RGDA 4
 RESULT 5
 US-10-050-692-3
 Sequence 3, Application US/10050692
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 FILE REFERENCE: 3033-1002-004
 CURRENT APPLICATION NUMBER: US/10/050,692
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fragment of human prothrombin
 US-10-050-692-3

Query Match	100.0%	Score 21;	DB 13;	Length 4;
Best Local Similarity	100.0%	Pred. No.	9.5e+05	
Matches	4	Conservative	0	Mismatches 0;
Qy	1 RGDA 4	Indels	0	Gaps 0;
Db	1 RGDA 4			

RESULT 6
 US-10-050-611-1
 Sequence 1, Application US/10050611
 Publication No. US20050187933A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 TITLE OF INVENTION: PEPTIDES
 FILE REFERENCE: 3033 1000 008
 CURRENT APPLICATION NUMBER: US/10/050,611
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/904,090
 PRIOR FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 60/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FASTSEQ FOR Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Human fragment of thrombin
 US-10-050-611-1

Query Match	100.0%	Score 21;	DB 13;	Length 4;
Best Local Similarity	100.0%	Pred. No.	9.5e+05	
Matches	4	Conservative	0	Mismatches 0;
Qy	1 RGDA 4	Indels	0	Gaps 0;
Db	1 RGDA 4			

RESULT 7
 US-10-050-688-3
 Sequence 3, Application US/10050688
 Publication No. US200501815A1
 GENERAL INFORMATION:
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
 TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
 FILE REFERENCE: 3033 1003 004
 CURRENT APPLICATION NUMBER: US/10/050,688
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,348
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,800
 PRIOR FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FASTSEQ FOR Windows Version 4.0
 SEQ ID NO 3

RESULT 8
 US-10-200-879-23
 Sequence 23, Application US/10200879
 Publication No. US2003014420A1
 GENERAL INFORMATION:
 APPLICANT: Hawley Nelson, Pamela
 LAN, Jianqiong
 SHIH, Pojnting
 SCHIFFERLI, Kevin P.
 GEBEYEHU, Guliat
 TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GREENLEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/200,879
 FILING DATE: 23-Jul-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/911,569
 FILING DATE: 23-JUL-2001
 APPLICATION NUMBER: US 09/039,780
 FILING DATE: 16-MAR-1998
 APPLICATION NUMBER: US 08/818,200
 FILING DATE: 14-MAR-1997
 APPLICATION NUMBER: US 08/658,130
 FILING DATE: 04-JUN-1996
 APPLICATION NUMBER: US 08/477,354
 ATTORNEY/AGENT INFORMATION:
 NAME: Sullivan, Sally A.
 REGISTRATION NUMBER: 32,064
 REFERENCE/DOCKET NUMBER: 32-95E
 TELECOMMUNICATION INFORMATION:
 PHONE: (303)499-8080
 FAX: (303)499-8089
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-200-879-23
 Query Match 100.0%; Score 21; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 670
 Qy 1 RGDA 4
 Db 1 RGDA 4
 ;
 RESULT 9
 US-09-989-789-289
 ; Sequence 289, Application US/09989789
 ;
 GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.20 / S11-US2
 ; CURRENT APPLICATION NUMBER: US/09/989,789
 ; CURRENT FILING DATE: 2002-03-25
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
 US-09-989-789-671
 Query Match 100.0%; Score 21; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 289
 Qy 1 RGDA 4
 Db 1 RGDA 4
 ;
 RESULT 12
 US-09-989-789-672
 ; Sequence 672, Application US/09989789
 ;
 GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.20 / S11-US2
 ; CURRENT APPLICATION NUMBER: US/09/989,789
 ; CURRENT FILING DATE: 2002-03-25
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 672
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
 US-09-989-789-672
 Query Match 100.0%; Score 21; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 289
 Qy 1 RGDA 4
 Db 1 RGDA 4
 ;
 RESULT 13
 US-09-989-789-673
 ; Sequence 673, Application US/09989789
 ;
 GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.20 / S11-US2
 ; CURRENT APPLICATION NUMBER: US/09/989,789
 ; CURRENT FILING DATE: 2002-03-25
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
 US-09-989-789-670
 Query Match 100.0%; Score 21; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 670
 Qy 1 RGDA 4
 Db 1 RGDA 4
 ;
 RESULT 11
 US-09-989-789-671
 ;

Search completed: March 18, 2004, 07:24:52
 Job time : 11.4762 secs

RESULT 14
 US-09-989-789-674
 Sequence 674, Application US/09989789
 Patent No. US20030063179A1
 GENERAL INFORMATION:
 APPLICANT: LIU, Qiang
 TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 FILE REFERENCE: 8325-0011.20 / S11-US2
 CURRENT APPLICATION NUMBER: US/09/989,789
 CURRENT FILING DATE: 2002-03-25
 NUMBER OF SEQ ID NOS: 4085
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 674
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: example ZFP
 US-09-989-789-674
 Query Match 100.0%; Score 21; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 15
 US-09-989-789-675
 Sequence 675, Application US/09989789
 Patent No. US20030063379A1
 GENERAL INFORMATION:
 APPLICANT: LIU, Qiang
 TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 FILE REFERENCE: 8325-0011.20 / S11-US2
 CURRENT APPLICATION NUMBER: US/09/989,789
 CURRENT FILING DATE: 2002-03-25
 NUMBER OF SEQ ID NOS: 4085
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 675
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: example ZFP
 US-09-989-789-675
 Query Match 100.0%; Score 21; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RGDA 4
 Db 1 RGDA 4

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OM protein - protein search, using SW model

Run on: March 18, 2004, 07:21:00 ; Search time 39 Seconds
(without alignments)

92.958 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71

Sequence: 1 RGDAAXGDSGGPXY 14

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Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 25895539 residues

Total number of hits satisfying chosen parameters: 7224

Minimum DB seq length: 14

Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listning first 45 summaries

Published Applications AA:
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 2: /cgm2_6_ptodata/1/pubpaa/bct_new_pub.pep:
 3: /cgm2_6_ptodata/1/pubpaa/us06_new_pub.pep:
 4: /cgm2_6_ptodata/1/pubpaa/us06_PUBCOMB.pep:
 5: /cgm2_6_ptodata/1/pubpaa/us07_new_pub.pep:
 6: /cgm2_6_ptodata/1/pubpaa/pcutus_PUBCOMB.pep:
 7: /cgm2_6_ptodata/1/pubpaa/us08_new_pub.pep:
 8: /cgm2_6_ptodata/1/pubpaa/us08_PUBCOMB.pep:
 9: /cgm2_6_ptodata/1/pubpaa/us09_PUBCOMB.pep:
 10: /cgm2_6_ptodata/1/pubpaa/us09c_PUBCOMB.pep:
 11: /cgm2_6_ptodata/1/pubpaa/us09c_PUBCOMB.pep:
 12: /cgm2_6_ptodata/1/pubpaa/us09c_new_pub.pep:
 13: /cgm2_6_ptodata/1/pubpaa/us10a_PUBCOMB.pep:
 14: /cgm2_6_ptodata/1/pubpaa/us10c_PUBCOMB.pep:
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 16: /cgm2_6_ptodata/1/pubpaa/us10c_new_pub.pep:
 17: /cgm2_6_ptodata/1/pubpaa/us60_new_pub.pep:
 18: /cgm2_6_ptodata/1/pubpaa/us60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	67	94.4	14	US-09-909-122-4
2	67	94.4	14	US-10-050-692-4
3	67	94.4	14	US-10-050-688-4
4	52	73.2	14	US-09-885-441-6
5	32	45.1	14	US-19-310-422B-20
6	32	45.1	14	US-10-311-558-31
7	30	42.3	14	US-10-341-979-8
8	27	38.0	14	US-19-880-748-3215
9	25	35.2	14	US-09-815-837-109
10	25	35.2	14	US-09-812-455-34
11	25	35.2	14	US-09-812-455-35
12	25	35.2	14	US-19-851-455-36
13	25	35.2	14	US-09-812-455-37
14	25	35.2	14	US-09-812-455-38
15	25	35.2	14	US-09-880-748-3218

Sequence 16, App1
Sequence 17, App1
Sequence 170, App1
Sequence 173, App1
Sequence 92, App1
Sequence 195, App1
Sequence 23, App1
Sequence 23, App1
Sequence 33, App1
Sequence 8, App1
Sequence 14, App1
Sequence 13, App1
Sequence 16, App1
Sequence 93, App1
Sequence 97, App1
Sequence 101, App1
Sequence 15, App1
Sequence 16, App1
Sequence 84, App1
Sequence 320, App1
Sequence 11, App1
Sequence 77, App1
Sequence 108, App1
Sequence 29, App1
Sequence 16, App1
Sequence 158, App1
Sequence 63, App1
Sequence 5, App1
Sequence 123, App1
Sequence 9, App1

ALIGNMENTS

RESULT 1
US-09-909-1122-4
; Sequence 4, Application US/09909122
; Patent No. US20030128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; CROWther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033 1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; PRIORITY FILING DATE: 2001-07-19
; PRIORITY APPLICATION NUMBER: US 60/219,300
; PRIORITY FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(14)
; OTHER INFORMATION: Xaa at position six is Glu or Gln
; OTHER INFORMATION: Xaa at position thirteen is Bhe, Met, Ieu, His or Val
; US-09-909-1122-4
Query Match Score 67; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0;
Matches 14; Conservative 0; Indels 0; Gaps 0;
CY 1 RGDAAXGDSGGPXY 14
DB 1 RGDAAXGDSGGPXY 14

RESULT 2
US-10-050-692-4
Sequence 4, Application US/10050692
Publication No. US20020182205A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
CROWTHER, Roger S.
SIMMONS, David J.
APPLICANT: Yang, Jinhang
REDIN, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES
FILE REFERENCE: 3033-1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 9/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fragment of human prothrombin
FEATURE:
NAME/KEY: VARIANT
LOCATION: (6) ..(6)
OTHER INFORMATION: Xaa = Glu or Gln
FEATURE:
NAME/KEY: VARIANT
LOCATION: (13) ..(13)
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-4
Query Match 94.4%; Score 67; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-698-4
Query Match 94.4%; Score 67; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Xaa = Glu or Gln
RESULT 4
US-09-885-441-6
Sequence 6, Application US/09885441
Patent No. US2002014640A1
GENERAL INFORMATION:
APPLICANT: XIAO, Yonghong
TITLE OF INVENTION: Regulation of Human Eosinophil Serine
Protease-1-Like Enzyme
FILE REFERENCE: 04974.00512
CURRENT APPLICATION NUMBER: US/09/885,441
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/212,844
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/244,171
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: US 60/279,766
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: BLOCKS domain
US-09-885-441-6
Query Match 73.2%; Score 52; DB 9; Length 14;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OTHER INFORMATION: BLOCKS domain
RESULT 5
US-09-300-425B-20
Sequence 20, Application US/09300425B
Publication No. US20030045681A1
GENERAL INFORMATION:
APPLICANT: TARLI, Lorenzo
VITI, Francesca
BIRCHLER, Manfred
APPLICANT: NERI, Dario
APPLICANT: CROWTHER, Roger S.
APPLICANT: STIERBERG, Janet
APPLICANT: BERGMANN, John
TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 3,033,1003-004
SEQUENCE 4, Application US/10050688
Publication No. US2002018154A1
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
TYPE: PRT
ORGANISM: Artificial Sequence
RESULT 6
US/09/300-425B
GENERAL INFORMATION:
APPLICANT: VITI, Francesca
BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIogenesis
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B

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; CURRENT FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIORITY FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: antibody linker
; OTHER INFORMATION: Description of Artificial Sequence: antibody linker

Query Match 45.1%; Score 32; DB 10; Length 14;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GDACKGDSGG 11
Db 1 GDGSSGSGGG 10

RESULT 8
US-09-980-748-3215
; Sequence 3215, Application US/09880748
; Publication No. US003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3215
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-980-748-3215

Query Match 42.3%; Score 30; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GDACKGDSGG 11
Db 5 GDEVGDSGG 14

RESULT 9
US-09-815-837-109
; Sequence 109, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Darrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Immune Mediators and Related Methods
; FILE REFERENCE: 01-058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; CURRENT FILING DATE: 2003-01-11
; PRIOR APPLICATION NUMBER: US 60/264,003

Query Match 38.0%; Score 27; DB 10; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GDSSGP 12
Db 7 GDSSGP 12

RESULT 7
US-10-341-979-8
; Sequence 8, Application US/10341979
; GENERAL INFORMATION:
; APPLICANT: Hong Kong University of Science & Technology
; APPLICANT: Chang, Donald Choy
; APPLICANT: Luo, Qian Kathy
; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
; FILE REFERENCE: 32.44183-1
; CURRENT APPLICATION NUMBER: US 10/341,979
; CURRENT FILING DATE: 2003-01-11
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR APPLICATION NUMBER: US 60/264,003
; CURRENT FILING DATE: 2003-01-11
; PRIOR APPLICATION NUMBER: US 60/264,003

```

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; PRIORITY FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 109
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cavia porcellus
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OTHER INFORMATION: Linker for C0580 and C0587
US-09-815-837-109

Query Match 35.2%; Score 25; DB 9; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
SEQ ID NO: 34
Qy 7 GDGGP 12
Db 7 GGGGP 12

RESULT 10
US-09-852-455-34
; Sequence 34, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: HSLAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-455-36

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
SEQ ID NO: 36
Qy 7 GDGGP 12
Db 1 GELGGP 6

RESULT 11
US-09-852-455-35
; Sequence 35, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: HSLAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-852-455-37

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;

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Qy 7 GDSGGP 12
Db 1 GELGGP 6

RESULT 14
US-09-852-455-38
Sequence 38 Application US/09812455
/ Publication No. US20010054348A1
/ GENERAL INFORMATION:
/ APPLICANT: BLOM, ARTHUR J.
/ GOLDSTEIN, NEIL
/ PILIJUTA, RENUKA
/ APPLICANT: HSIAO, KC-CHUAN
/ PRENDERGAST, JOHN
/ TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
/ CURRENT APPLICATION NUMBER: US/09/852,455
/ FILE REFERENCE: 2598-4004US1
/ CURRENT FILING DATE: 2001-05-09
/ PRIOR FILING DATE: 2000-05-09
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 38
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Felis catus
US-09-852-455-38

Qy 7 GDSGGP 12
Db 1 GELGGP 6

RESULT 15
US-09-880-748-3218
/ Sequence 3218 Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immuno specifically Bind Blys
/ FILE REFERENCE: PP523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 3218
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-3218

Qy 1 RGDAKXGDSG 10

Search completed: March 18, 2004, 07:27:53
Job time : 40 secs

Qy 2 RPDADYGDYG 11

RESULT 2
 US-10-050-692-4
 Sequence 4 Application US/10050692
 Publication No. US20020182205A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 CROWther, Roger S.
 SIMMONS, David J.
 APPLICANT: Yang, Jinping
 REDIN, William R.
 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 TITLE OF INVENTION: PEPTIDE DERIVATIVES
 FILE REFERENCE: 3033-1002-004
 CURRENT APPLICATION NUMBER: US/10/050,692
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/903,122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: fragment of human prothrombin
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (6) ..(6)
 OTHER INFORMATION: Xaa = Glu or Gln
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (13) ..(13)
 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
 US-10-050-692-4
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: fragment of human prothrombin
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (6) ..(6)
 OTHER INFORMATION: Xaa = Glu or Gln
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (13) ..(13)
 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
 US-10-050-692-4
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence

RESULT 3
 US-10-050-688-4
 Sequence 4 Application US/10050688
 Publication No. US20020198154A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 CROWther, Roger S.
 APPLICANT: Bergman, John
 STIERBERG, Janet
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH NON-PROTEOLYTICALLY ACTIVATED THROMBIN
 TITLE OF INVENTION: RECEPTOR AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
 FILE REFERENCE: 3033-1003-004
 CURRENT APPLICATION NUMBER: US/10/050,688
 PRIOR APPLICATION NUMBER: 09/309,348
 CURRENT FILING DATE: 2002-01-16
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 09/309,348
 CURRENT FILING DATE: 2000-07-20
 PRIOR FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence

RESULT 4
 US-09-777-328-8
 Sequence 8 Application US/09777328
 Patent No. US2002032314A1
 GENERAL INFORMATION:
 APPLICANT: CAREY, DARRELL H.
 CAREY, Roger S.
 PAMAKITSHAN, SYAM
 TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
 FILE REFERENCE: CBP:002
 CURRENT APPLICATION NUMBER: US/09/777,328
 CURRENT FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: 08/330,594
 PRIOR FILING DATE: 1994-10-28
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 8
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-777-328-8
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 8
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-777-328-8
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 8
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-777-328-8
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 8
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence

RESULT 5
 US-09-904 090-3
 Sequence 3 Application US/09904090
 Publication No. US20020061852A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell
 CAREY, Roger S.
 TITLE OF INVENTION: PEPTIDES OF THERAPY WITH THROMBIN DERIVED
 FILE REFERENCE: 3033-1000-001
 CURRENT APPLICATION NUMBER: US/09/904,090
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: US 60/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-050-3

Query Match 94.4%; Score 67; DB 9; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;

Qy 1 RGDAAXGDGGPKV 14
Db 10 RGDAECEGDSGGPPFV 23

RESULT 6
US-10-050-692-6

Sequence 6, Application US/10050692
Publication No. US2002018205A1

GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, JinPeng
APPLICANT: Redin, William R.

TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN

FILE REFERENCE: 3033.1002-004

CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SEQ ID NO: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: C-terminal amidated fragment of human thrombin

NAME/KEY: AMIDATION
LOCATION: (23) . . . (23)

OTHER INFORMATION: valine is amidated as CONH2

US-10-050-692-6

Query Match 94.4%; Score 67; DB 13; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;

Qy 1 RGDAAXGDGGPKV 14
Db 10 RGDAECEGDSGGPPFV 23

RESULT 7
US-10-050-611-3

Sequence 3, Application US/10050611
Publication No. US2002018793A1

GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED

FILE REFERENCE: 3033.1000-008
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 3

Length: 23
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: human fragment of thrombin

OTHER INFORMATION: human fragment of thrombin
US-10-050-611-3

Query Match 94.4%; Score 67; DB 13; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;

Qy 1 RGDAAXGDGGPKV 14
Db 10 RGDAECEGDSGGPPFV 23

RESULT 8
US-10-050-611-4

Sequence 4, Application US/10050611
Publication No. US2002018793A1

GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED

FILE REFERENCE: 3033.1000-008
CURRENT APPLICATION NUMBER: US/10/050,611
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: c-terminal amidated fragment of human thrombin

NAME/KEY: AMIDATION
LOCATION: (23) . . . (23)

OTHER INFORMATION: valine is amidated as CONH2

US-10-050-611-4

Query Match 94.4%; Score 67; DB 13; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;

Qy 1 RGDAAXGDGGPKV 14
Db 10 RGDAECEGDSGGPPFV 23

RESULT 9
US-10-050-688-5

Sequence 5, Application US/10050688
Publication No. US2002019815A1

GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Siernberg, Janet
APPLICANT: Bergmann, John

TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOYTICALLY ACTIVATED THROMBIN

FILE REFERENCE: 3033.1000-008
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 3

NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of thrombin
US-10-050-688-5
Query Match 94.4%; Score 67; DB 13; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RGDA^CXGDSGPXV 14
Db 10 RGDA^CE^DGSGGP^FV 23

RESULT 10
US-10-050-688-6
Sequence 6, Application US/10050688
; Publication No. US/020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stermberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033-1003-004
; CURRENT APPLICATION NUMBER: US/10/050-688
; CURRENT FILING DATE: 2002-11-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of thrombin
; NAME/KEY: AMIDATION
; LOCATION: (23) . (23)
; OTHER INFORMATION: CONH2
US-10-050-688-6
Query Match 94.4%; Score 67; DB 13; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RGDA^CXGDSGPXV 14
Db 10 RGDA^CE^DGSGGP^FV 23

RESULT 11
US-09-909-348-5
Sequence 5, Application US/0909348
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stermberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH With Agonists
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: 3033-1003-001
; CURRENT APPLICATION NUMBER: US/020042373A1

RESULT 12
US-09-909-122-5
Sequence 5, Application US/0909122
; Patent No. US/0020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033-1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/909,122
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-5
Query Match 94.4%; Score 67; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RGDA^CXGDSGPXV 14
Db 12 RGDA^CE^DGSGGP^FV 25

RESULT 13
US-10-050-692-5
Sequence 5, Application US/10050692
; Publication No. US/2002018205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033-1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692

RESULT 14
US-09-909-348-4
Sequence 5, Application US/0909348
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stermberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: 3033-1003-001
; CURRENT APPLICATION NUMBER: US/10/050,692

CURRENT FILING DATE: 2002-01-16
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US20030077691A1
; PRIOR FILING DATE: 2000-07-19, 3000
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-5

Query Match 94.4%; Score 67; DB 13; Length 25;
Best Local Similarity 85.7%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGDA~~C~~XGDSGPXV 14
Db 12 RGDA~~C~~EGDSSGP~~F~~V 25

RESULT 15
US-09-898-837A-41
; Sequence 41, Application US/09898837A
; Publication No. US20030077691A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerr E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majunder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: Curagen Corporation
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R.
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
; PRIOR FILING DATE: 2000-02-19
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
; PRIOR FILING DATE: 2000-07-03
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 41
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-898-837A-41

Query Match 94.4%; Score 67; DB 10; Length 251;
Best Local Similarity 85.7%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 198 RGDA~~C~~EGDSSGP~~F~~V 211

Search completed: March 18, 2004, 07:24:52
Job time : 36.6667 secs

Query Match 94.4%; Score 67; DB 10; Length 250;
SEQ ID NO: 45
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-898-837A-45

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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:22:05 ; search time 39 Seconds
 165.997 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141

Sequence: 1 AGTRYRPDEGKRGDACEGDSGGPFV 25

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 25

Maximum DB seq length: 25

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing First 45 summaries

Published Applications AA,*

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  6: /cgns_6/ptodata/1/pubpaas_pctus_pubcomb.pep:*
  7: /cgns_6/ptodata/1/pubpaas_usos_pubcomb.pep:*
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  13: /cgns_6/ptodata/1/pubpaas_us09_pubcomb.pep:*
  14: /cgns_6/ptodata/1/pubpaas_us10_pubcomb.pep:*
  15: /cgns_6/ptodata/1/pubpaas_us10c_pubcomb.pep:*
  16: /cgns_6/ptodata/1/pubpaas_us10_new_pub.pep:*
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  18: /cgns_6/ptodata/1/pubpaas/us60_pubcomb.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	100.0	25	9	US-09-909-348-5
2	141	100.0	25	9	US-09-909-122-5
3	141	100.0	25	13	US-10-050-692-5
4	38	27.0	25	15	US-10-353-522A-1
5	36	25.5	25	9	US-09-864-761-3798
6	33	23.4	25	9	US-09-864-761-4392
7	31	22.3	25	14	US-10-233-471-1059
8	31	22.0	25	10	US-09-852-455-75
9	31	22.0	25	10	US-09-962-156-1099
10	31	22.0	25	14	US-10-13-128-205
11	31	22.0	25	15	US-10-389-660-205
12	31	22.0	25	15	US-10-233-471-1059
13	31	22.0	25	16	US-10-53-493-1099
14	30	21.3	25	10	US-09-33-767-598
15	30	21.3	25	13	US-10-036-869-7

Sequence 598, APP Sequence 11, APP Sequence 409, APP Sequence 4594, A Sequence 555, APP Sequence 219, APP Sequence 23, APP Sequence 3, APP Sequence 256, APP Sequence 3, APP1 Sequence 11, APP Sequence 312, APP Sequence 314, APP Sequence 31, APP1 Sequence 4557, A Sequence 322, APP Sequence 263, APP Sequence 362, APP Sequence 118, APP Sequence 28, APP1 Sequence 31, APP1 Sequence 118, APP Sequence 31, APP1 Sequence 362, APP Sequence 16, APP1 Sequence 313, APP Sequence 119, APP

ALIGNMENTS

RESULT 1

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; Sequence 5, Application US/09909348
; Patent No. US2002042373A1
; GENERAL INFORMATION:
;   APPLICANT: Carney, Darrell H.
;   CROWTHORPE, Roger S.
;   SCIERBERG, Janet
;   BERGMANN, John
;   INVENTION: Stimulation Of Cartilage Growth With Agonists
;   OF THE NO. US2002042373A1-Proteolytically Activated Thrombin Re-
;   FILE REFERENCE: 3033 NUMBER: US/09/909-348
;   CURRENT APPLICATION NUMBER: US 60/219,880
;   PRIORITY FILING DATE: 2001-07-19
;   PRIORITY NUMBER: US 2002042373A1
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO: 5
;   LENGTH: 25
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     OTHER INFORMATION: Peptide Fragment of Thrombin
;     US-09-909-348-5

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Query Match Score 141; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.2e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTRYKPDEGKRGDACEGDSGGPFV 25
 Db 1 AGTRYKPDEGKRGDACEGDSGGPFV 25

RESULT 2

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; Sequence 1099, APP Sequence 1099, APP Sequence 598, APP Sequence 7, APP
; Sequence 5, Application US/09909122
; Sequence 11, APP Sequence 312, APP Sequence 314, APP Sequence 31, APP1
; Sequence 4557, A Sequence 322, APP Sequence 263, APP Sequence 362, APP Sequence 118, APP Sequence 28, APP1 Sequence 31, APP1 Sequence 118, APP Sequence 31, APP1 Sequence 362, APP Sequence 16, APP1 Sequence 313, APP Sequence 119, APP

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Patent No. US20020128202A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinpang
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 FILE REFERENCE: 3033-1002-001
 CURRENT APPLICATION NUMBER: US 09/909,122
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 6/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 5
 SEQ ID NO 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide Fragment of Thrombin
 US-09-909-122-5

Query Match 100.0%; Score 141; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6 2e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTRYKPDEGKRGDAECDGGPFV 25
 Db 1 AGTRYKPDEGKRGDAECDGGPFV 25

RESULT 3
 US-10-050-692-5
 Sequence 5 Application US/10050692
 Publication No. US20020182205A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinpang
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 FILE REFERENCE: 3033-1002-004
 CURRENT APPLICATION NUMBER: US/10/050,692
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 6/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 6
 SEQ ID NO 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fragment of human prothrombin
 US-10-050-692-5

Query Match 100.0%; Score 141; DB 13; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.2e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTRYKPDEGKRGDAECDGGPFV 25
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RESULT 4
 US-10-353-522A-1

; Sequence 1, Application US/10353522A
 ; Publication No. US2003016298A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walgen Pharmaceuticals, Inc.
 ; APPLICANT: Park, Jong-Gu
 ; APPLICANT: Moon, Ik-Jae
 ; APPLICANT: Kim, Young-Cheol
 ; TITLE OF INVENTION: Peptide for Increasing Transfection Efficiency
 ; FILE REFERENCE: 57354-13USA
 ; CURRENT APPLICATION NUMBER: US 10/353,522A
 ; CURRENT FILING DATE: 2003-01-28
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: artificial
 ; FEATURE:
 ; OTHER INFORMATION: RGD-RGD-TatC-RGD-RGD
 US-10-353-522A-1

Query Match 27.0%; Score 38; DB 15; Length 25;
 Best Local Similarity 40.0%; Pred. No. 3.2e+01;
 Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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 Db 5 GDRXKRQRQQRRPQQCRERG 24

RESULT 5
 US-09-864-761-37498
 Sequence 37498, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Perrin, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wenshang
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeonica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263,6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 6/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 37498
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011504.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.5
; OTHER INFORMATION: SWISSPROT HIT: P22857, EVALUATE 1.70e+00
US-09-864-761-37498          Score 36; DB 9; Length 25;
Query Match      Best Local Similarity 66.7%; Pred. No. 5.9e+02; Indels 1; Mismatches 2; Gaps 0;
Db               15 ACEGDGGG 23
Db               11 ACQSRSGGp 19

RESULT 6
US-09-864-761-43492
; Sequence 43492, Application US/09864761
; Patent No. US20030048763A1
; GENERAL INFORMATION:
;   APPLICANT: Penn, Sharron G.
;   APPLICANT: Rank, David R.
;   APPLICANT: Hanzel, David K.
;   APPLICANT: Chen, Weipeng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-13
; PRIOR APPLICATION NUMBER: GB 24253.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

RESULT 7
US-10-280-066-233
; Sequence 233, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
;   APPLICANT: Pillutla, Renuka C.
;   APPLICANT: Brissette, Renee
;   APPLICANT: Spruyt, Michael
;   APPLICANT: Dadoya, Olga
;   APPLICANT: Blume, Arthur J.
;   APPLICANT: Prendergast, John T.
;   APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINDING
; FILE REFERENCE: 2398-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 233
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: 07902-DG12-20M-PP-BC-CS
US-10-280-066-233          Score 22.3%; DB 9.5; Length 25;
Query Match      Best Local Similarity 52.9%; Pred. No. 2.3e+01; Mismatches 7; Indels 1; Gaps 1;
Qy

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Db 10 AGFRLYRGADDRGD-CE 25 RESULT 8 US-09-852-455-75 Sequence 75, Application US/09852455 Publication No. US20030054348A1 GENERAL INFORMATION: / APPLICANT: BLUME, ARTHUR J. / APPLICANT: GOLDSTEIN, NEIL / APPLICANT: PILLUTTA, RENUKA / APPLICANT: HSIAO, KU-CHUAN / APPLICANT: PRENDERGAST, JOHN TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS FILE REFERENCE: 2598-4004US1 CURRENT APPLICATION NUMBER: US/09/852,455 PRIOR APPLICATION NUMBER: 60/105-09 PRIOR FILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 81 SEQ ID NO: 75 LENGTH: 25 TYPE: PRT ORGANISM: Homo sapiens us-09-852-455-75 Query Match 22.0%; Score 31; DB 10; Length 25; Best Local Similarity 57.1%; Pred. No. 2.7e+03; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0; Gaps 0; Qy 18 GDSGGPFV 24 Db 16 GEAGGGY 22

RESULT 10 US-10-133-128-205 Sequence 205, Application US/10133128 GENERAL INFORMATION: / APPLICANT: KOLMAN, JOOST A. / APPLICANT: STEMMER, WILLEM P.C. / TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS CURRENT APPLICATION NUMBER: US/10/133,128 CURRENT FILING DATE: 2002-04-26 PRIORITY APPLICATION NUMBER: 60/374,107 PRIORITY FILING DATE: 2002-04-18 PRIORITY APPLICATION NUMBER: 60/333,359 PRIORITY FILING DATE: 2001-11-16 PRIORITY APPLICATION NUMBER: 60/337,209 PRIORITY FILING DATE: 2001-11-19 PRIORITY APPLICATION NUMBER: 60/286,623 PRIORITY FILING DATE: 2001-04-26 NUMBER OF SEQ ID NOS: 244 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO: 205 LENGTH: 25 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic NAME/KEY: misc_feature LOCATION: (1)-(12) OTHER INFORMATION: This region may vary in length from 1-12 residues OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues FEATURE: NAME/KEY: misc_feature LOCATION: (14)-(25) OTHER INFORMATION: This region may vary in length from 1-12 residues OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues US-10-133-128-205

Query Match 22.0%; Score 31; DB 14; Length 25; Best Local Similarity 46.2%; Pred. No. 2.7e+03; Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0; Gaps 0; Qy 10 GKRGDAECDSGG 22 Db 7 GGGGGGGGGGGG 19

RESULT 11 US-10-289-660-205 Sequence 205, Application US/10289660 GENERAL INFORMATION: / APPLICANT: KOLMAN, JOOST A. / APPLICANT: STEMMER, WILLEM P.C. / APPLICANT: GOVINDARAJAN, SRIDHAR / TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS CURRENT APPLICATION NUMBER: 0319-510US CURRENT FILING DATE: 2003-11-06 PRIORITY APPLICATION NUMBER: US/10/289,660 PRIORITY APPLICATION NUMBER: 10/133,128

Db 1099 LENGTH: 25 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide FEATURE: NAME/KEY: MOD_RES LOCATION: (13) OTHER INFORMATION: Unknown amino acid; translation read-through at TGA stop codon OTHER INFORMATION: TGA stop codon

PRIOR FILING DATE: 2002-04-26
 PRIOR APPLICATION NUMBER: 60/374,107
 PRIOR FILING DATE: 2002-04-18
 PRIOR APPLICATION NUMBER: 60/333,359
 PRIOR FILING DATE: 2001-11-26
 PRIOR APPLICATION NUMBER: 60/337,209
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/286,823
 NUMBER OF SEQ ID NOS: 244
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 205
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: peptide linker
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(12)
 OTHER INFORMATION: This region may vary in length from 1-12 residues,
 OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
 FEATURE:
 NAME/KEY: (14)..(25)
 LOCATION: (14)..(25)
 OTHER INFORMATION: This region may vary in length from 1-12 residues,
 OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
 US-10-289-660-205
 Query Match Score 31; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 2.7e+03;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 10 GKGDAEKGDSGG 22
 Db 7 GGGGGGGGGGGGG 19

RESULT 12
 US-10-253-471-1099
 Sequence 1099, Application US/10253471
 Publication No. US200302336190A1
 GENERAL INFORMATION:
 APPLICANT: PILLUTIA, RENUKA et al.
 TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 FILE REFERENCE: 1878-4057
 CURRENT APPLICATION NUMBER: US/10/253,471
 CURRENT FILING DATE: 2002-09-24
 PRIOR APPLICATION NUMBER: 09/962,756
 PRIOR FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: 09/538,038
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/146,127
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 2227
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1099
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Unknown amino acid; translation read-through at
 LOCATION: (13)
 OTHER INFORMATION: Unknown amino acid; translation read-through at
 US-10-253-471-1099
 Query Match Score 31; DB 15; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 18 GDGGPF 24
 Db 16 GEAGGPY 22

RESULT 13
 US-10-253-493-1099
 Sequence 1099, Application US/10253493
 Publication No. US20040023887A1
 GENERAL INFORMATION:
 APPLICANT: PILLUTIA, RENUKA et al.
 TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 FILE REFERENCE: 1878-4056
 CURRENT APPLICATION NUMBER: US/10/253,493
 CURRENT FILING DATE: 2002-09-24
 PRIOR APPLICATION NUMBER: 09/962,756
 PRIOR FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: 09/538,038
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/146,127
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 2227
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1099
 LENGTH: 25
 TYPE: PPT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (13)
 OTHER INFORMATION: Unknown amino acid; translation read-through at
 US-10-253-493-1099
 Query Match Score 31; DB 16; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 18 GDGGPF 24
 Db 16 GEAGGPY 22

RESULT 14
 US-09-933-767-598
 Sequence 598, Application US/099333767
 Publication No. US200301692A1
 GENERAL INFORMATION:
 APPLICANT: NI et al.
 TITLE OF INVENTION: Human Secreted Proteins
 FILE REFERENCE: PZ007P2
 CURRENT APPLICATION NUMBER: US/09/933,767
 CURRENT FILING DATE: 2001-08-22
 PRIOR APPLICATION NUMBER: PC/PUS01/05614
 PRIOR FILING DATE: 2001-02-21
 PRIOR APPLICATION NUMBER: 60/184,836
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/193,170
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/205,258
 PRIOR FILING DATE: 1998-12-04
 PRIOR APPLICATION NUMBER: PCT/US98/11422
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/048,885
 PRIOR FILING DATE: 1997-06-06
 PRIOR APPLICATION NUMBER: 60/049,375
 PRIOR FILING DATE: 1997-06-06
 PRIOR APPLICATION NUMBER: 60/048,881

Query Match Score 31; DB 15; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;

; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-4613
; INFORMATION FOR SEQ ID NO: 7;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
us-10-036-869-7

Query Match Score 30; DB 13; Length 25;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
Db 2 GTRYKDEGKRGDAACEGDSSG 21
Qy | :| | | | | | | | | | | | | | | | | | |
Db 4 GSRGKSYIGSRGKSYIGSRG 23

Search completed: March 18, 2004, 07:28:45
Job time : 40 secs

CURRENT FILING DATE: 2002-01-16
 PRIORITY APPLICATION NUMBER: 09/904,090
 PRIOR FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: US10/050,688
 PRIOR FILING DATE: 2000-07-12
 PRIOR APPLICATION NUMBER: 09/909,348
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: human fragment of thrombin
 US-10-050-611-3

Query Match 85.8%; Score 121; DB 13; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 21; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 5 YKPDEGKRGDAECDGGPPV 25
 Db 3 YKPDEGKRGDAECDGGPPV 23

RESULT 7
 US-10-050-611-4
 Sequence 4, Application US/10050611
 Publication No. US2002018933A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 PEPTIDES

CURRENT APPLICATION NUMBER: US/10/050,611
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/904,090
 PRIOR FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 09/909,348
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: c-terminal amidated fragment of human thrombin
 NAME/KEY: AMIDATION
 LOCATION: 23
 OTHER INFORMATION: valine is amidated as CONH2
 US-10-050-611-4

Query Match 85.8%; Score 121; DB 13; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 21; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 5 YKPDEGKRGDAECDGGPPV 25
 Db 3 YKPDEGKRGDAECDGGPPV 23

RESULT 8
 US-10-050-688-5
 Sequence 5, Application US/10050688
 Publication No. US20020198154A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN

Query Match 85.8%; Score 121; DB 13; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 21; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 5 YKPDEGKRGDAECDGGPPV 25
 Db 3 YKPDEGKRGDAECDGGPPV 23

RESULT 10
 US-10-165-442-2
 Sequence 2, Application US/10165442
 Publication No. US2003015440A1
 GENERAL INFORMATION:
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN

```

; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1) .. (259)
; OTHER INFORMATION: Thrombin W215A B-Chain
US-10-165-442-2

Query Match 85.8%; Score 121; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 YKPDEGKRGDACEGDSGGPFV 25
Db 190 YKPDEGKRGDACEGDSGGPFV 210

RESULT 13
US-10-165-442-3

Query Match 85.8%; Score 121; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 YKPDEGKRGDACEGDSGGPFV 25
Db 226 YKPDEGKRGDACEGDSGGPFV 246

; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 3
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1) .. (36)
; OTHER INFORMATION: Thrombin W8 A-Chain
US-10-165-442-4

Query Match 81.8%; Score 121; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 YKPDEGKRGDACEGDSGGPFV 25
Db 226 YKPDEGKRGDACEGDSGGPFV 246

; GENERAL INFORMATION:
; APPLICANT: McCarthy, Allen
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MM-002
; CURRENT APPLICATION NUMBER: US/10/020,141
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/313,097
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/327,485
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 295
; TYPE: PRT
US-10-020-141-8

Query Match 81.8%; Score 121; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 YKPDEGKRGDACEGDSGGPFV 25
Db 226 YKPDEGKRGDACEGDSGGPFV 246

; GENERAL INFORMATION:
; APPLICANT: Ableson, Allen
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MM-002
; CURRENT APPLICATION NUMBER: US/10/020,141
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/313,097
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/327,485
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 295
; TYPE: PRT
US-10-020-141-8

Query Match 81.8%; Score 121; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 YKPDEGKRGDACEGDSGGPFV 25
Db 226 YKPDEGKRGDACEGDSGGPFV 246

; GENERAL INFORMATION:
; APPLICANT: McCarthy, Allen
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MM-002
; CURRENT APPLICATION NUMBER: US/10/020,141
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/313,097
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/327,485
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 295
; TYPE: PRT
US-10-020-141-8

```

```

; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-00-14-8

Query Match          85.8%; Score 121; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      5 YKPDEGRGKRGDACEGDSGGPPV 25
Db      553 YKPDEGRGKRGDACEGDSGGPPV 573

RESULT 15
US-10-017-631-2
; Sequence 2, Application US/10017631
; Publication No. US2003009957A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-006
; CURRENT APPLICATION NUMBER: US/10/017,631
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/325,930
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 622
; TYPE: PRI
; ORGANISM: Homo sapiens
US-10-017-631-2

Query Match          85.8%; Score 121; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      5 YKPDEGRGKRGDACEGDSGGPPV 25
Db      553 YKPDEGRGKRGDACEGDSGGPPV 573

```

Search completed: March 18, 2004, 07:24:53
Job time : 66.4762 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:17:19 ; Search time 13.5 Seconds
(without alignments)
71.253 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CBGDSGGPFV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 311

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR 78:
1: Pir1:
2: Pir2:
3: Pir3:
4: Pir4:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	39.0	10	XGHUE	erythrocyte membra
2	20	33.9	10	PH027	T-cell receptor be
3	20	33.9	10	PH025	T-cell receptor be
4	19	32.2	10	PH094	T-cell receptor be
5	18	30.5	10	C39572	sperm-activating p
6	18	30.5	10	B60589	sperm-activating p
7	17	28.8	10	BA9581	sialokinin II - ye
8	17	28.8	10	C61440	polygalacturonase
9	17	28.8	10	PH134	Tg heavy chain DJ
10	17	28.8	10	PT0622	T-cell receptor be
11	17	28.8	10	PT064	T-cell receptor be
12	16	27.1	10	PE6087	sperm-activating p
13	16	27.1	10	D60527	sperm-activating p
14	16	27.1	10	PN015	sperm-activating p
15	16	27.1	10	E39572	triose-phosphate i
16	16	27.1	10	F60589	acetylcholinester
17	16	27.1	10	D60589	Ig heavy chain CRD
18	16	27.1	10	E60589	T-cell receptor be
19	16	27.1	10	A60588	T-cell receptor ga
20	16	27.1	10	PN015	cytochrome P450 1A
21	16	27.1	10	A24136	tachykinin I - mig
22	16	27.1	10	PT0243	T-cell receptor al
23	16	27.1	10	PT0215	angiotensin-conver
24	16	27.1	10	B41946	mannose receptor -
25	16	27.1	10	PH0903	
26	15	25.4	10	ECLQIM	
27	15	25.4	10	S23371	
28	14	23.7	10	XASNPC	
29	14	23.7	10	S39374	

311

RESULT 1

XGHUE erythrocyte membrane glycopeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A03187

R;Reiss, J.B.; Lote, C.J.; Bobinski, H.

Nature New Biol. 234, 25-26, 1971

A;Title: New low molecular weight glycopeptide containing triglucosylcysteine in human e

A;Reference number: A03187; PMID:72034940; MUID:5266858

A;Accession: A03187

A;Molecule type: protein

A;Residues: 1-10 <WET>

C;Comment: The identity of the glycoprotein from which this peptide is derived is unknown

found (see PIR:XCHUEU).

C;Superfamily: unsigned animal peptides

F:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query	Match	Score	DB	Length	10;
Qy	Matches	Best Local Similarity	Conservative	Mismatches	1; Indels 0; Gaps 0;
1	1	39.0	XGHUE	5	
2	1	33.9	PH027	5	

Query	Match	Score	DB	Length	10;
Qy	Matches	Best Local Similarity	Conservative	Mismatches	1; Indels 0; Gaps 0;
1	1	39.0	XGHUE	5	
2	1	33.9	PH027	5	
3	1	32.2	PH025	5	
4	1	30.5	PH094	5	
5	1	30.5	C39572	5	
6	1	28.8	B60589	5	
7	1	28.8	BA9581	5	
8	1	28.8	C61440	5	
9	1	28.8	PH134	5	
10	1	28.8	PT0622	5	
11	1	28.8	PT064	5	
12	1	27.1	PE6087	5	
13	1	27.1	D60527	5	
14	1	27.1	PN015	5	
15	1	27.1	E39572	5	
16	1	27.1	F60589	5	
17	1	27.1	D60589	5	
18	1	27.1	E60589	5	
19	1	27.1	A60588	5	
20	1	27.1	PN015	5	
21	1	27.1	A24136	5	
22	1	27.1	PT0243	5	
23	1	27.1	PT0215	5	
24	1	27.1	B41946	5	
25	1	27.1	PH0903	5	
26	1	25.4	ECLQIM	5	
27	1	25.4	S23371	5	
28	1	23.7	XASNPC	5	
29	1	23.7	S39374	5	

Query	Match	Score	DB	Length	10;
Qy	Matches	Best Local Similarity	Conservative	Mismatches	1; Indels 0; Gaps 0;
1	1	39.0%	XGHUE	5	
2	1	30.0%	PH0927	5	
3	1	29.0%	R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.	5	
4	1	29.0%	J. Exp. Med. 174, 1467-1476, 1991	5	
5	1	29.0%	A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis	5	
6	1	29.0%	A;Reference number: PH0891; MUID:92078857; PMID:18336012	5	
7	1	29.0%	A;Accession: PH0927	5	
8	1	29.0%	A;Molecule type: T-cell receptor	5	
9	1	29.0%	A;Residues: 1-10 <GCL>	5	
10	1	29.0%	A;Experimental source: concanavalin A-activated lymphoblast	5	
11	1	29.0%	C;Keywords: T-cell receptor	5	
12	1	29.0%	Query	5	
13	1	29.0%	Match	3	
14	1	29.0%	Best Local Similarity	1	
15	1	29.0%	Conservative	1	
16	1	29.0%	Mismatches	1	
17	1	29.0%	Indels	0	
18	1	29.0%	Gaps	0	

RESULT 3
 PH0925 T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991.
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0925
 A;Molecule type: mRNA
 A;Residues: 1-10 <GOL>
 A;Experimental source: concanavalin A-activated lymphoblast
 C;Keywords: T-cell receptor

Query Match 33.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 42.9%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Indels 0; Gaps 0;

Qy 1 CEGDSGG 7
 Db 1 CASSDGG 7

RESULT 4
 PH0944 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991.
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0944
 A;Molecule type: mRNA
 A;Residues: 1-10 <GOL>
 A;Experimental source: complete Freund's adjuvant-immunized lymph node
 A;Note: the authors translated the codon GAC for residue 9 as Glu
 C;Keywords: T-cell receptor

Query Match 32.2%; Score 19; DB 2; Length 10;
 Best Local Similarity 42.9%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Indels 0; Gaps 0;

Qy 1 CEGDSGG 7
 Db 1 CASSPGG 7

RESULT 5
 C39572 sperm-activating peptide TG-3 - sea urchin (*Tripneustes gratilla*)
 N;Alternate names: speract homolog TG-3
 C;Species: *Tripneustes gratilla*
 C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000
 C;Accession: C39572
 R;Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Shioya, T.; Biochemistry 30, 6203-6209, 1991.
 A;Title: Identification of a novel amino acid, O-bromo-L-phenylalanine, in egg-associate protein
 A;Reference number: A39572; MUID:91283461; PMID:2059627
 A;Accession: C39572
 A;Molecule type: protein
 A;Residues: 1-10 <XOS>
 C;Superfamily: unassigned animal peptides
 C;Keywords: bromine
 F;Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match 30.5%; Score 18; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Indels 0; Gaps 0;

Qy 4 DSAGGG 7
 Db 5 DGGGG 8

RESULT 6
 B60589 sperm-activating peptide (GLY-3, Ser-5, Ile-9 SAP-I) - slate-pencil urchin (Heterocentrotus mamillatus)
 C;Species: Heterocentrotus mamillatus
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: B60589
 R;Yoshino, K.T.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimoniishi, Y.; Kurita, M.; Yamaguchi, Comp. Biochem. Physiol. B 94, 739-751, 1989.
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related peptide otus nudus, *Echinometra mathaei* and *Heterocentrotus mamillatus*.
 A;Accession number: A65277
 A;Reference number: A65277
 A;Molecule type: protein
 A;Residues: 1-10 <XOS>
 C;Superfamily: unassigned animal peptides

Query Match 30.5%; Score 18; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.9e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSSGG 7
 Db 3 GLSGGG 7

RESULT 7
 B49581 *Sialokinin II* - yellow fever mosquito
 C;Species: *Aedes aegypti* (yellow fever mosquito)
 C;Date: 05-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000
 C;Accession: B49581
 R;Champagne, D.E.; Ribeiro, J.M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994.
 A;Title: *Sialokinin I* and *II*: vasodilatory tachykinins from the yellow fever mosquito *Ae. A;Accession number: A49581; MUID:94105119; PMID:8278354
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <CHA>
 A;Experimental source: Rockefeller, salivary gland
 A;Note: sequence extracted from NCBI backbone (NCBIP:141842)
 C;Superfamily: unassigned animal peptides*

Query Match 28.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 7.2e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DSGGPPF 9
 Db 1 DTGDKF 6

RESULT 8
 C61440 polygalacturonase (EC 3.2.1.15) II b - *Aspergillus* sp. (fragment)
 C;Species: *Aspergillus* sp.
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996
 C;Accession: C61440
 R;Stratilova, E.; Markovic, S.; Skrovnova, D.; Rexova-Benkova, L.; Jornvall, H.
 J. Protein Chem. 12, 15-22, 1993.
 A;Title: Pectinase *Aspergillus* sp. Polygalacturonase: multiplicity, divergence, and structure
 A;Accession number: A61440; MUID:93151962; PMID:8427629
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <STR>
 C;Keywords: Glycosidase; hydrolase; polysaccharide degradation

Db 3 DLGG 6

RESULT 14

E39572 sperm-activating peptide TG-5 - sea urchin (*Tripneustes gratilla*)

N;Alternate names: spact homolog TG-5

C;Species: *Tripneustes gratilla*

C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000

C;Accession: E39572

R;Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh

Biochemistry 30: 6203-6205, 1991

A;Title: Identification of a novel amino acid, α -bromo-L-phenylalanine, in egg-associate

A;Reference number: A39572; MUID:91283461; PMID:2059627

A;Accession: E39572

A;Molecule type: protein

A;Residues: 1-10 <YOS>

C;Superfamily: unassigned animal peptides

C;Keywords: bromine

F;2/Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match 27.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 5 SGG 7
Db 5 |||
 5 SGG 7

RESULT 15

F60589 sperm-activating peptide (Asn-3, Ser-5 SAP-I) - *Echinometra mathaei* (type A)C;Species: *Echinometra mathaei*

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C;Accession: F60589

R;Yoshino, K.I.; Kaijura, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguc

Comp. Biochem. Physiol. B 94, 739-751, 1989

A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe

otus indicus, *Echinometra mathaei* and *Heterocentrotus mammillatus*.

A;Reference number: A60527

A;Accession: F60589

A;Molecule type: protein

A;Residues: 1-10 <YOS>

C;Superfamily: unassigned animal peptides

Query Match 27.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 5 SGG 7
Db 5 |||
 5 SGG 7Search completed: February 26, 2004, 09:24:05
Job time : 14.5 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
SUMMARIES							
SwissProt_42:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	120						
Total number of hits satisfying chosen parameters:							
Minimum DB seq length: 10							
Maximum DB seq length: 10							
Post-processing: Minimum Match 100%							
Database : SwissProt_42:*							
Scoring table: BLOSUM62							
Gapop 10.0 , Gapext 0.5							
Searched: 141681 seqs, 52070155 residues							
Total number of hits satisfying chosen parameters:	120						
Minimum DB seq length: 10							
Maximum DB seq length: 10							
Post-processing: Minimum Match 100%							
Listing first 45 summaries							

RESULT 1							
ID	GIEM_HUMAN	STANDARD;	PRT;	10 AA.			
AC	P02728;				DT	21-JUL-1986 (Rel. 01, Created)	
					DT	21-JUL-1986 (Rel. 01, Last sequence update)	
					DT	16-OCT-2001 (Rel. 40, Last annotation update)	
					DE	Brythrocyte membrane Glycopeptide.	
					OS	Homo sapiens (Human)	
					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buterida; Primates; Catarrhini; Hominidae; Homo.	
					OX	NCBI_TAXID=9606;	
					RN	[1]	
					RP	SEQUENCE.	
					RX	MEDLINE=7034940; PubMed=5286858;	
					RA	Weiss J.B., Lotz C.J., Bobinski H.	
					RT	"New low molecular weight Glycopeptide containing trigluicosylcysteine in human erythrocyte membrane";	
					RL	Nature New Biol. 234:25-26 (1971).	
					CC	-!- PBM: S-linked Glycan consists of GIC-Glc-Glc trisaccharide.	
					CC	-!- MISCLEANEOS: The identity of the glycoprotein from which this peptide is derived is unknown. No physiological function has been attributed.	
					CC	CC peptide is derived is unknown. No physiological function has been attributed.	
					DR	PIR; A03187; XGHUE.	
					RW	Glycoprotein; Erythrocyte.	
					FT	CARBOPROTEIN 1	S-LINKED (GLC.).
					SQ	SEQUENCE 10 AA; 1049 MW; 239BPBAAF5B1E8 CRC64;	
					Query Match	39.04%; Score 23; DB 1; Length 10;	
					Best Local Similarity	80.0%; Pred. No. 2e+02; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
					Qy	1 CIEGDS 5	
					Db	1 CBBHS 5	

RESULT 2							
ID	FARS_PANRE	STANDARD;	PRT;	10 AA.			
AC	P02660;				DT	16-OCT-2001 (Rel. 40, Created)	
					DT	16-OCT-2001 (Rel. 40, Last sequence update)	
					DT	16-OCT-2001 (Rel. 40, Last annotation update)	
					DE	FMRFamilyde-1-like neuropeptide PF6 (NGRPQPFVRF-amide).	
					OS	Panagrellus redivivus.	
					OC	Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Paragrellida; Panagrellida; Panagrotaimidae; Panagrellus; NCBI_TAXID=6333;	
					OX		
					RN	[1]	
					RP	SEQUENCE, FUNCTION, AND AMIDATION.	
					RA	Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G., Maile A.G.,	
					RA	RA	
					RT	-!- Isolation, characterization and pharmacology of RMRFamilyde-related peptides (FAPs) from free living nematode, Panagrellus redivivus ";	
					RT	peptides (FAPs) from free living nematode, Panagrellus redivivus "	
					RL	Submitted (JUL-2000) to Swiss-Prote.	

-!- FUNCTION: Myoactive.
 CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 MW; AMIDATION
 SQ TKS2_AEDAE 10 AA; CB13E4C9D776C76D CRC64;

Query Match Score 17; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PFV 10
 Db 6 PFV 8

RESULT 3
TKS2_AEDAE STANDARD; PRT; 10 AA.
 ID TKS2_AEDAE
 AC P42633;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Sialokinin II.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 OX NCBI_TaxID:7159;
 RN [1]
 RP SEQUENCE.
 SEQUENCE=Rockefeller; TISSUE=Salivary gland;
 MEDLINE=P42633;
 RA Champagne D.E., Ribeiro J.M.C./
 Champigne D.E., Ribeiro J.M.C./
 RT mosquito Aedes aegypti.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
 -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the
 site of feeding.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the Tachykinin family.
 DR PIR; B49581; B49811.
 DR InterPro; IPR000040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 MOD_RES 10 MW; AMIDATION.
 SQ SEQUENCE 10 AA; 1146 MW; 30C77C8B59C33AA8 CRC64;

Query Match Score 17; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DSGPFF 9
 Db 1 DRGDKF 6

RESULT 4
ESTA_SCIGA STANDARD; PRT; 10 AA.
 ID ESTA_SCIGA
 AC P81012;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 15-JUL-1998 (Rel. 36; Last annotation update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 (Fragment).
 OS Schizaphis graminum (Aphid).
 OC Schizaphis graminum (Aphid); Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Neoponera; Hemiptera; Sternorrhyncha; Aphidoidea;
 Aphidoidea; Aphidiidae; Aphidini; Schizaphis.
 NCBI_TaxID:13262;
 RN [1]
 RP SEQUENCE; MEDLINE=37468499; PubMed=9327586;

RX

RA Siegfried B.D., Ono M., Swanson J.J.;
 RT "Purification and characterization of a carboxylesterase associated
 with organophosphate resistance in the greenbug, *Schizaphis graminum*
 (Homoptera: Aphididae)".
 RT Arch. Insect Biochem. Physiol. 36:229-240 (1997).
 -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 carboxylic anion.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC Intero.; IPR000018; Carboxylesterases_B_1; PARTIAL.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1;
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
 KW Hydrolase; Serine esterase.
 FT NON_TER 10 MW; 018AB587865A2CO CRC64;
 SQ SEQUENCE 10 AA; 1025 MW; 018AB587865A2CO CRC64;

Query Match Score 16; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SGG 7
 Db 5 SGG 7

RESULT 5
COKX_RABIT STANDARD; PRT;
 ID COKX_RABIT
 AC P80336;
 DT 01-OCT-1994 (Rel. 30; Created)
 DT 01-OCT-1994 (Rel. 30; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
 (Fragment).
 GN COKXH.
 OS Oryctolagus cuniculus (Rabbit).
 RA Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae;
 NCBI_TaxID=9986;
 OX [1]
 RN RN
 RP SEQUENCE.
 TISSUE=Heart, and Liver;
 RC Friend R.; Kadenbach B.;
 RA Submitted (MAR-1994) to Swiss-Prot.
 RL Submitted (MAR-1994) to Swiss-Prot.
 -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 chains of cytochrome c oxidase, the terminal oxidase in
 mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
 KW Oxidoreductase; Mitochondrion.
 FT NON_TER 10 MW; 2C325CB40DC76338 CRC64;
 SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match Score 15; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SGGP 8
 Db 2 SGKP 5

RESULT 6
BPP_VIPAS STANDARD; PRT;
 ID BPP_VIPAS
 AC P31351;
 DT 01-JUL-1993 (Rel. 26; Created)
 DT 01-FEB-1994 (Rel. 28; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Bradykinin-potentiating Peptide (Angiotensin-converting
 enzyme inhibitor)
 DE Vipera aspis (Aspic viper).
 OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8706;
 RN [1]
 RP
 RC TISSUE=venom;
 RX MEDLINE=9038616; PubMed=2169439;
 RA Konoi Y., Sugihara H.; "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of *Vipera aspis aspis*.";
 RT Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the activation of bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 CC PIR; A6377; XASNFC.
 DR KW Hypotensive; agent; Pyrrolidone carboxylic acid.
 FT MOD RBS 1_1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match. Score 14; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 7.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; .

Qy 7 GPFV 10
 Db 5 GPKV 8

RESULT 7
 RCA_PINPS STANDARD; PRT; 10 AA.
 AC P8184;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable ribulose bisphosphate carboxylase/oxygenase activase (RuBisCO activase) (RA) (Water stress responsive protein 4) (Fragment).
 DE Pinus pinaster (Maritime pine).
 OS Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 OC Spermatophytina; Coniferopsida; Coniferales; Pinaceae; Pinus.
 RN [1]
 RP
 RC TISSUE=Needle;
 RX MEDLINE=99418576; PubMed=9747804;
 RA Costa P., Bahman N., Frigerio J.-M., Kremer A., Flomion C., i
 RT "Water-deficit-responsive proteins in maritime pine.";
 RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubois C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Flomion C.;
 RT "Separation and characterization of needle and xylem maritime pine proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- FUNCTION: Activation of RuBisCO (ribulose-1,5-bisphosphate carboxylase/oxygenase; EC 4.1.1.39) involves the ATP-dependent carboxylation of the epsilon-amino group of lysine leading to a carbamate structure (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
 CC -!- INDUCTION: By water stress.
 CC -!- SIMILARITY: Belongs to the RuBisCO activase family.
 CC Chloroplast; ATP-binding.
 FT NON_TER 1_1
 SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1EA6 CRC64;

Query Match. Score 14; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;

CC -!- SIMILARITY: Belongs to the serpin family.
DR PIR; A90315; A90345;
DR JERCS; 3JUL-92;
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 10 10 ANGIOTENSIN III.

SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PF 9
Db 7 PF 8

RESULT 10
ANGT_CHICK STANDARD; PRT; 10 AA.
AC P01018;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 02, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin III)] (Fragment).
DE AGT OR SERPINAB.
OS Gallus gallus (Chicken); and
Coturnix coturnix japonica (Japanese Quail).
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC OX NCBI_TaxID=9031; 93934;
RN SPECIES=C.c.japonica;
RP SEQUENCE.
RC SPECIES=Chicken;
RX MEDLINE=90284684; PubMed=4361802;
RA Nakayama T.; Nakajima T.; Sckabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
angiotensin and its identification by DNS-method.";
RT Chem. Pharm. Bull.; 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.c.japonica;
RX MEDLINE=90284684; PubMed=2191893;
RT Inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol.; 7:1-2-22(1990).
CC -!- FUNCTION: In response to lowered blood pressure, the enzyme renin
cleaves angiotensin I, from angiotensinogen. ACT (angiotensin
converting enzyme) then removes a dipeptide to yield the
physiologically active peptide angiotensin II, the most potent
pressor substance known, which helps regulate volume and mineral
balance of body fluids.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Expressed by the liver and secreted in plasma.
CC -!- SPECIFICITY: Belongs to the serpin family.
PIR; A60624; A60634.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 10 10 ANGIOTENSIN III.

SEQUENCE , 10 AA; 1232 MW; CEEFBDD761F2DB42 CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PF 9
Db 7 PF 8

RESULT 11
COXO_RAT STANDARD; PRT; 10 AA.
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIc, mitochondrial (EC 1.9.3.1)
DE COX7C OR COX7CL.
GN COX7C OR COX7CL.
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC SPBAIN_Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=95324529; PubMed=601105;
RA Schaegger H.; Noack H.; Halangk W.; Brandt U.; von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
amino-terminal sequences suggest identity of the fetal heart and the
adult liver isozyme.", Eur. J. Biochem. 230:235-241(1995).
RT RL -!- FUNCTION: this protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferricytochrome
CC C + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIc family.
DR PIR; S63388; S65388.
KW Oxidoreductase; Mitochondrion.
FT NON_TBR 10 10
SQ SEQUENCE 10 AA; 1117 MW; 12DDE767687B1B0B CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GP 8
Db 6 GP 7

RESULT 12
COXO_THUB STANDARD; PRT; 10 AA.
AC P80582;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIc (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC BukaToya; Merazoa; Chordata; Craniata; Vertebrata; Euteleostei; Teleostei; Neoteleostei; Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Scombroidei; Acanthomorpha; Acanthopterygii; Perciformes; Perciformia; Perciformes; Scombrodei; Scombridae; Thunnius.
NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RX MEDLINE=97454391; PubMed=9310366;
RA Arnold S.; Lee I.; Kim M.; Song E.; Linder D.; Lottepeich F.;
RA Kaderbach B.;

"The subunit structure of cytochrome-c oxidase from tuna heart and liver." Eur. J. Biochem. 248:99-103(1997).
 RL CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyanocochrome c + O₂) = 4 ferricytochrome c + 2 H⁺O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
 DR PIR; S77930; S77939.
 DR Oxidoreductase; Inner membrane; Mitochondrion.
 KW FT NON_TER 10
 SQ SEQUENCE 10 AA; 1059 MW;
 Query Match 22.0%; Score 13; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GP 8
 Db 6 GP 7

RESULT 13
 PNEU_HUMAN STANDARD; PRT; 10 AA.
 AC P22103;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DE Pneumadin (PNN).
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN SEQUENCE.

RP TISSUE=Lung;
 RC MEDLINE=91110910; PubMed=2274681;
 RX RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
 RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
 RL Regul. Pept. 30:77-87(1990).
 CC -!- FUNCTION: Antidiuretic peptide that triggers the release of ADH.
 DR PIR; A33143; A33143.
 DR MOD_RES 10 AA; 10 AMIDATION.

FT SEQ 10 AA; 646 MW;

Query Match 22.0%; Score 13; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.2e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSG 6
 Db 7 DAG 9

RESULT 14
 PNEU_RAT STANDARD; PRT; 10 AA.
 AC P21936;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pneumadin (PNN).
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NCBI_TaxID=10116;
 RN SEQUENCE, AND SYNTHESIS.

RP TISSUE=Lung;
 RC MEDLINE=91110910; PubMed=2274681;
 RX RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
 RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
 RL Regul. Pept. 30:77-87(1990).
 CC -!- FUNCTION: This antidiuretic peptide triggers the release of ADH.
 DR PIR; A33143; A33143.
 DR MOD_RES 10 AA; 10 AMIDATION.

FT SEQ 10 AA; 64100D0AA723276B CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.2e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PYF 10
 Db 4 PYI 6

Search completed: February 26, 2004, 09:22:04
 Job time : 12.5 secs

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 603

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREML25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_nitric:*

8: sp_organelle:*

9: sp_oxygen:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:

17: sp_archeap:*

Run on: February 26, 2004, 09:16:49 (without alignments)
Perfect score: 59
Sequence: 1 CEGDGGPFV 10

Title: US-09-909-348-1

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Run on: February 26, 2004, 09:16:49 (without alignments)
Perfect score: 90.148 Million cell updates/sec

Q95936 beta vulgaris sp. pro
Q9QVF0 mus sp. pro
Q9QVF9 mus sp. pro
Q9QVF9 homo sapien
P84222 bombyx mori
Q8M78 bos mutus g.
Q92113 aegilops sp.
Q8JF1 pseudomorpha
Q9rJ8 helicobacte
Q9rJ8 homo sapien
Q9rJ8 homo sapien
Q8A22 homo sapien
Q8B93 brookesia p.
Q8B93 rhampholeon
Q85492 pyrrhobryon
Q9593 silene pent
Q9y0 brassica ju
Q93389 rattus norvegicus
Q83978 influenzae
P9037 suis herpes
Q9PY8 triakis scyane
Q9Y93 gallus gallus
Q9y07 alligator mississippiensis
Q9pru9 sparus aurata
Q7594 gallus gallus
Q8KAN9 clostridium
Q52837 rhizobium
Q51812 escherichia coli
Q9uct6 homo sapien
Q725a2 homo sapien

ALIGNMENTS

RESULT 1

ID	PB2938	PRELIMINARY;	PRT;	10 AA.
AC	PB2938;			
DT	01-MAR-2001 (TRIMBLrel. 16, Created)			
DT	01-MAR-2001 (TRIMBLrel. 16, Last sequence update)			
DI	01-JUN-2001 (TRIMBLrel. 17, Last annotation update)			
DB	Unknown endosperm protein C (Fragment).			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplanteae; Streptophytina; Embryophytina; Tracheophytina;			
OC	Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Pooideae;			
OC	Triticeae; Hordeum.			
NCBI_TaxID	4513;			
RN	[1]			
RP	RPL STRAIN=CV. BOMI; TISSUE=Starchy endosperm;			
RC	Medline=2108891; PubMed=11271488;			
RA	Kristoffersen H.B.; Flengsrød R.;			
RT	"Separation and characterization of basic barley seed proteins."			
RL	Electrophoresis 21:3693-3700 (2000).			
CC	-1-MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 8.5-10. ITS MW IS: 11.9 KDA.			
FT	NON TER 10 10			
SEQUENCE	10 AA; 1053 MW;	9E562DC040AA87AAE CRC64;		

Query Match Score 39.0%; Score 23; DB 10; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+03; Mismatches 1; Indels 0; Gaps 0;

Qy CEGD 4
Db CDGD 6

RESULT 2

Result No.	Score	Query Match	Length	DB ID	Description
1	23	39.0	10	P82938	P82938 hordeum vulgare
2	20	33.9	10	Q0032	Q0032 mycobacteri
3	20	33.9	10	Q9T542	Q9T542 sus scrofa
4	18	30.5	10	Q9NF2	Q9NF2 homo sapien
5	18	30.5	10	Q9QVK7	Q9QVK7 mus sp. mep
6	17	28.8	10	Q9X533	Q9X533 escherichia
7	17	28.8	10	Q9X534	Q9X534 leclercia
8	17	28.8	10	Q9EB86	Q9EB86 homo sapien
9	16	27.1	10	Q947R7	Q947R7 solanum tuberosum
10	16	27.1	10	Q9TU33	Q9TU33 canis familiaris
11	16	27.1	10	Q82136	Q82136 spinacia ol
12	16	27.1	10	Q8CU31	Q8CU31 mus musculus
13	15	25.4	10	Q93M2	Q93M2 prochlorococcus
14	15	25.4	10	Q96QY9	Q96QY9 homo sapien
15	15	25.4	10	Q8BEY9	Q8BEY9 homo sapien
16	15	25.4	10	Q95229	Q95229 homo sapien

DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01; Last annotation update)
 DE Mycobacterium leprae.
 OS Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1] _SEQUENCE FROM N.A.
 RP Smith D.R.;
 RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2] _SEQUENCE FROM N.A.
 RP Robinson K.;
 RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U15182; AAA62915.1; -.
 SEQUENCE 10 AA; 1137 MW;
 Query Match 33.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Prd. No. 5.9e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 Qy 1 CCG 3
 Db - 6 CCG 8
 PRT; 10 AA.

RESULT 3
 Q9TS42_ PRELIMINARY;
 ID Q9TS42_ PRELIMINARY;
 AC DT 01-MAY-2000 (TREMBLrel. 13; Created)
 DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 22; Last annotation update)
 DE OESTRADIOL-RECEPTOR=P2 peptide (Fragment).
 OS Sus scrofa (Pig).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=9823;
 RN SEQUENCE FROM N.A.; PubMed=2064608;
 RX RA Thole H.H.; Jungblut P.W.; Jakob F.;
 RT "The proton-driven dissociation of oestradiol-receptor dimers as a
 preparative tool. Isolation of a 32 kDa fragment from porcine uteri
 and assignment of C-terminal origin by partial sequencing.";
 RL Biochem J. 276:709-714(1991).
 FT NON_TER 1 1
 FT 10 10
 SEQUENCE 10 AA; 992 MW; D95E047B1451B76D CRC64;

Query Match 33.9%; Score 20; DB 6; Length 10;
 Best Local Similarity 60.0%; Prd. No. 5.9e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
 Q9X53_ PRELIMINARY;
 ID Q9X53_ PRELIMINARY;
 AC DT 01-NOV-1999 (TREMBLrel. 12; Created)
 DT 01-NOV-1999 (TREMBLrel. 12; Last sequence update)
 DE Periplasmic mercuric ion binding protein (Fragment).
 GN MERP
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1] _SEQUENCE FROM N.A.
 RP STRAIN=209A;
 RC MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A.; Wierman J.; Smith T.; Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of Gram-negative
 bacteria isolated from the fecal flora of primates.";
 OX NCBI_TaxID=9606;

RESULT 4
 Q9JNPF2_ PRELIMINARY;
 ID Q9JNPF2_ PRELIMINARY;
 AC DT 01-MAY-2000 (TREMBLrel. 13; Created)
 DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)
 DE Alpha-1 collagen (Fragment).
 GN COL1A1
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=209A;
 RX MEDLINE=9807386; PubMed=9361435;
 RA Liebert C.A., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 gram-negative fecal bacteria of primates";
 RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=209A;
 RX MEDLINE=20568355; PubMed=1116334;
 RA Liebert C.A., Watson A.L., Summers A.O.;
 RT "The quality of merc, a module of the mer mosaic.";
 RL J. Mol. Evol. 51:607-622 (2000).
 DR AF120964; ADD2383.1; -.
 FT NON-TER 1 1
 SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;
 QY 4 DSGGP 8
 DB 1 DAGYP 5

RESULT 7
 ID Q9X534 PRELIMINARY; PRT; 10 AA.
 AC Q9X534;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE periplasmic mercuric ion binding protein (Fragment).
 GN MERP.
 OS Leclercia adecarboxylata.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Leclercia.
 NCBI_TaxID=83655;
 OX [1]

RP SEQUENCE FROM N.A.
 RN SEQUENCE FROM N.A.
 RC STRAIN=42H;
 RX MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A., Wierman J., Smith T., Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 bacteria isolated from the fecal flora of primates.";
 RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=742H;
 RX MEDLINE=98027386; PubMed=9361435;
 RA Liebert C.A., Wierman J., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 gram-negative fecal bacteria of primates.";
 RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=742H;
 RX MEDLINE=20568355; PubMed=1116334;
 RA Liebert C.A., Watson A.L., Summers A.O.;
 RT "The quality of merc, a module of the mer mosaic.";
 RL J. Mol. Evol. 51:607-622 (2000).
 FT NON-TER 1 1
 SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;
 QY 26.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; Misnches 1; Indels 0; Gaps 0;

QY 4 DSGGP 8
 DB 1 DAGYP 5

RESULT 8
 ID Q9UE86 PRELIMINARY; PRT; 10 AA.
 AC Q9UE86;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Collagen alpha 1(I) chain (Fragment).
 GN COL1AI.
 OS Homo sapiens (Human).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 OX [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=12042176; PubMed=11939261;
 RA Hawkins J.R., Superti-Surga A.; Steinmann B.; Dalgleish R.;
 RT "A 9-base pair deletion in COL1AI in a lethal variant of osteogenesis
 imperfecta.";
 RL J. Biol. Chem. 266:22370-22374 (1991).
 DR EMBL; S66556; AAB20361.1; -.
 DR GO; GO:0005584; C:collagen type I; NAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
 DR GO; GO:0007155; P:cell adhesion; NAS.
 FT NON-TER 1 1
 SQ SEQUENCE 10 AA; 777 MW; 2D20B6D8676DD867 CRC64;

QY 28.8%; Score 17; DB 4; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2e+04;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GDSGGP 8
 DB 1 GPPGAP 6

RESULT 9
 ID Q947R7 PRELIMINARY; PRT; 10 AA.
 AC Q947R7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 2, Last annotation update)
 DE SKT1 Potassium channel (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophytai; Embryophytai; Tracheophytai;
 OC Spermatophytai; Magnoliopsida; eudicots; eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 NCBI_TaxID=4113; OX [1]

RP SEQUENCE FROM N.A.
 RA Zimmerman S., Hartje S., Ehrlhardt T., Flesch G., Mueller-Roeber B.;
 RT "Two K⁺-inward rectifiers; SKM1 and KST1, co-assemble in potato guard
 cells via their C-terminal interaction domain.";
 RL Submitted (FEB-2000) to the ENSEMBL/GenBank/DDBJ databases.
 DR EMBL; AF231951; AAL13169.1; -.
 DR GO; GO:000516; F:ion channel activity; IEA.
 KW Ionic channel.
 FT NON-TER 10 10
 SQ SEQUENCE 10 AA; 1031 MW; 84F6E172864043A CRC64;

QY 26.8%; Score 17; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2e+04;
 Matches 3; Conservative 1; Mismatches 1; Misnches 1; Indels 0; Gaps 0;

QY 3 GDSGG 7
 DB 1 1

		Query Match Score 16;	DB 8;	Length 10;	
		Best Local Similarity 66.7%;	Pred. No. 2.9e+04;		
		Matches 2;	Mismatches 1;	Indels 0;	Gaps 0;
RESULT 10					
Db	2 GDNRG 6				
Q9TU33	PRELIMINARY;	PRT;	10 AA.		
ID Q9TU33					
AC Q9TU33; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE BRCA1 (Fragment).					
OS Canis familiaris (Dog).					
NCBItaxID=9615;					
OX Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Nematoda; Eutheria; Carnivora; Pissipedia; Canidae; Canis.					
[1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=20154965; PubMed=10690375;					
RA Gray J.S., Yuzbaşyan-Gurkan V.; MEDLINE=10690375;					
RT "A single nucleotide (T--G) polymorphism within intron 23 of the canine BRCA1 gene.";					
RL Anim. Genet. 31:16-17(2000).					
DR EMBL: AF159258; ADD56289; 1; -.					
FT NON_TER 10 10					
SQ SEQUENCE 10 AA; 1164 MN; 2AB89C65BAAB01B3 CRC64;					
Query Match Score 16%; DB 6; Length 10;					
Best Local Similarity 100.0%; Pred. No. 2.9e+04;					
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 4 DSG 6					
Db 6 DSG 8					
RESULT 11					
P81136	PRELIMINARY;	PRT;	10 AA.		
ID P81136					
AC P81136; DT 01-JUN-2000 (TREMBLrel. 14, Created) DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update) DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)					
DE Chloroplast 30S ribosomal protein S18 beta (Fragment).					
OS Spinacia olaracea (Spinach).					
OG Chloroplast.					
OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina.					
CC PROKARYOTAE: Magnoliophyta; eudicots; core eudicots;					
CC Caryophyllales; Amaranthaceae; Spinacia.					
NCBItaxID=3562;					
OX [1]					
RP SEQUENCE.					
STRAIN=cv. ALWARO; TISSUE=Leaf;					
RX MEDLINE=20435797; PubMed=1074039;					
RA Yamaguchi K., von Knoblauch K. Subramanian A.R.; "The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast)."; RT "Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";					
RT "Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";					
RL J. Biol. Chem. 37:28455-28455 (2000).					
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.					
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.					
CC -1- MISCELLANEOUS: S18 ALPHA AND BETA FORMS DIFFER IN PI.					
CC FORM IS THE LEAST BASIC FORM.					
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 kDa.					
CC -1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.					
CC GO: GO:0009507; CChloroplast; IEA.					
DR GO: GO:000035; Structural constituent of ribosome; IEA.					
DR InterPro: IPR001647; Ribosomal S18.					
DR PROSITE: PS00057; RIBOSOMAL_S18; PARTIAL.					
KW Ribosomal protein, Chloroplast.					
FT NON_TER 10 10 AA;					
SQ SEQUENCE 1250 MW; 403B60D7740325B3 CRC64;					

Query Match Score 15; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.3e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Search completed: February 26, 2004, 09:23:28
 Job time : 39 secs

Qy 2 EGDSG 6
 Db 5 QGSG 9

Db 3 CGSYCGG 9

RESULT 14

Q96Qa7	SEQUENCE	10 AA;	1076 MW;	75CA5CB05866D324 CRC64;
ID	Q96Qa7	PRELIMINARY;	PRT;	10 AA.
AC	Q96Qa7;			
DT	01-OCT-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DB	BA15A2.1 (Cddc42 Guanine exchange factor (GEF) 9 (Collybistin, PEM-2, ARHGEF9, HPEM-2, KIAA0424)) (Fragment).			
GN	Homo sapiens (Human)			
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo.			
OC				
OC				
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Whitehead S.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.			
RL	EMBL; AL451106; CAC84408.1;			
DR				
FT	NON_TER 10 10			
FT	SEQUENCE 10 AA; 1122 MW;			
SQ	39925CE878640043 CRC64;			

Query Match Score 15; DB 4; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSG 6
 Db 6 GSSG 9

Db 1 CGDGG 7

RESULT 15

QBNEY9	SEQUENCE	10 AA;	1034 MW;	9B53417EAB45B87E CRC64;
ID	QBNEY9	PRELIMINARY;	PRT;	10 AA.
AC	QBNEY9;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Type II hair-specific keratin (Fragment).			
GN	KRTHB6.			
OS	Homo sapiens (Human)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo.			
OC				
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bairwa N.K., Bamezai R.; "Study of polymorphism in the regulatory region of KRTHB6 in moniletrix samples," Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.			
RL	EMBL; A037532; ARK6868.1;			
DR	GO:0005882; C:intermediate filament; IEA.			
KW	Keratin.			
FT	NON_TER 10 10 AA;			
FT	SEQUENCE 10 AA; 1034 MW;			
SQ	9B53417EAB45B87E CRC64;			

Query Match Score 15; DB 4; Length 10;
 Best Local Similarity 42.9%; Pred. No. 4.3e+04;
 Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CEGDGG 7

Result No.	Score	Query Match Length	DB ID	Description
1	59	100.0	10 5	Aau73372 Serine es
2	59	100.0	10 5	AAE20155 Serine es
3	59	100.0	10 7	ABB80261 Serine es
4	46	78.0	10 5	AAU78373 Serine es
5	46	78.0	10 5	AAU20156 Serine es
6	46	78.0	10 7	ABB80262 Serine es
7	43	72.9	10 4	AB335464 Serine es
8	34	57.6	10 4	AAG94412 Human mem
9	31	52.5	10 4	Aaj01260 Hepatitis A
10	30	50.8	10 2	Aar1594 Peptide F
11	30	50.8	10 4	Aaj00701 Hepatitis A
12	30	50.8	10 4	Aaj01934 Hepatitis A
13	30	50.8	10 4	Aaj01082 Hepatitis A
14	29	49.2	10 2	AAR11746 Cyclic P1
15	29	49.2	10 2	AAR11747 Cyclic P1
16	29	49.2	10 2	AAR96844 N-Gonorrheal protein
17	29	49.2	10 2	Aaw79650 N-alpha-A
18	29	49.2	10 2	Aaw79652 N-alpha-A
19	29	49.2	10 2	Aaw79651 N-alpha-A
20	29	49.2	10 6	ABR26751 Human can
21	29	49.2	10 6	ABR26505 Human can
22	29	49.2	10 6	ABR26550 Human can
23	29	49.2	10 6	ABR26549 Human can
24	29	49.2	10 6	ABR25893 Human can
25	28	47.5	10 7	AAG97390 Human com

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM Protein - Protein search, using SW model
Run on: February 26, 2004, 09:00:54 ; Search time 48.5 Seconds
Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDGGPFV 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 946556

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04;*

- 1: GeneseqP1980;*
- 2: GeneseqP1990;*
- 3: GeneseqP2000s;*
- 4: GeneseqP2001s;*
- 5: GeneseqP2002s;*
- 6: GeneseqP2003s;*
- 7: GeneseqP2003s;*
- 8: GeneseqP2004s;*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	59	100.0	10 5	Aau73372 Serine es
2	59	100.0	10 5	AAE20155 Serine es
3	59	100.0	10 7	ABB80261 Serine es
4	46	78.0	10 5	AAU78373 Serine es
5	46	78.0	10 5	AAU20156 Serine es
6	46	78.0	10 7	ABB80262 Serine es
7	43	72.9	10 4	AB335464 Serine es
8	34	57.6	10 4	AAG94412 Human mem
9	31	52.5	10 4	Aaj01260 Hepatitis A
10	30	50.8	10 2	Aar1594 Peptide F
11	30	50.8	10 4	Aaj00701 Hepatitis A
12	30	50.8	10 4	Aaj01934 Hepatitis A
13	30	50.8	10 4	Aaj01082 Hepatitis A
14	29	49.2	10 2	AAR11746 Cyclic P1
15	29	49.2	10 2	AAR11747 Cyclic P1
16	29	49.2	10 2	AAR96844 N-Gonorrheal protein
17	29	49.2	10 2	Aaw79650 N-alpha-A
18	29	49.2	10 2	Aaw79652 N-alpha-A
19	29	49.2	10 2	Aaw79651 N-alpha-A
20	29	49.2	10 6	ABR26751 Human can
21	29	49.2	10 6	ABR26505 Human can
22	29	49.2	10 6	ABR26550 Human can
23	29	49.2	10 6	ABR26549 Human can
24	29	49.2	10 6	ABR25893 Human can
25	28	47.5	10 4	AAG97390 Human com

ALIGNMENTS

RESULT 1	ID	AAU73372 standard; peptide: 10 AA.
XX	AAU73372;	
XX	AC	
XX	DT	18-JUN-2002 (first entry)
DE		Serine esterase conserved sequence #1.
XX		Serine esterase; osteopathic; thrombin; receptor; agonist;
XX		KW bone growth stimulation; osteoinduction; farm animal; companion animal;
XX		KW laboratory animal; bone graft; segmental bone gap; bone void;
XX		KW non-union fracture.
OS		Synthetic.
XX	PN	WO200205836-A2.
XX	PD	24-JAN-2002.
XX	PD	24-JUL-2001; 2001IWO-US022641.
XX	PR	19-JUL-2000; 2000US-0219300P.
XX	PA	(TEXA) UNIV TEXAS SYSTEM.
XX	PI	Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR.
XX	DR	WPI; 2002-30376/34.
XX	WPI	WPI; 2002-30376/34.
CC	CC	The invention describes a method of stimulating bone growth at a site in a subject in need of osteoinduction, such as site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated thrombin receptor.
CC	CC	Claim 6; Page 21: 27pp; English.
CC	CC	The invention describes a method of stimulating bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoinduction, such as the site in a subject, a bone graft, a bone void or a non-union fracture. This sequence represents a serine esterase conserved sequence obtained from a serine esterase that can stimulate or activate the non-proteolytically activated thrombin receptor.
CC	CC	Sequence 10 AA;

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /label= Glu, Gln

FT Misc-difference 9 /label= Phe, Met, Leu, His, Val

XX WO200205836-A2.

XX PD 31-JAN-2002.

XX PR 19-JUL-2001; 2001WO-US022668.

XX PR 20-JUL-2000; 2000US-0219803P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Carney DH, Crowther RS, Stieremberg J, Bergmann J;

XX DR WPI; 2002-268953/31.

XX XX Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteolytically activated thrombin receptor.

XX PS Claim 9; Page 25; 28pp; English.

XX CC The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (NPTR). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPTR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is serine esterase conserved Peptide. This sequence is present in the thrombin peptide derivatives which serve as a NPTR agonist

XX SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 5; Length 10;

Best Local Similarity 80.0%; Pred. No. 6.9;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CEGDSGGPV 10
1 ||||| |
1 CXGDSGGPXY 10

DB

RESULT 6

ABB80562 ABB80562 standard; peptide; 10 AA.

XX ID ABB80562

XX AC ABB80562;

XX DT 18-DEC-2003 (First entry)

XX DE Serine esterase conserved sequence #2.

XX KW Serine esterase; conserved domain; thrombin peptide; stimulation; bone; cartilage; growth; repair; bone graft; segmental gap; bone void; non-union fracture; arthritic joint; arthritis; damage; traumatic injury; culture; chondrocyte; joint bio mechanics; osteoarthritis.

XX OS Mammal sp.

XX PH Key Misc-difference 2

XX FT /label= Glu, Gln

XX FT Misc-difference 9 /label= Phe, Met, Leu, His, Val

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PN Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;

XX PI

OS Sequence 10 AA;

Query Match 78.0%; Score 46; DB 5; Length 10;

Best Local Similarity 80.0%; Pred. No. 6.9;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CEGDSGGPV 10
1 ||||| |
1 CXGDSGGPXY 10

DB

RESULT 5

AAE20156 AAE20156 standard; peptide; 10 AA.

XX ID AAE20156

XX AC AAE20156;

XX DT 18-JUN-2002 (First entry)

XX DE Serine esterase conserved peptide #2.

XX KW Cartilage growth; cartilage repair; arthritic joint; traumatic injury; non-proteolytically activated thrombin receptor; NPTR; chondrocyte; therapy; implantation; serine esterase conserved peptide.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 2 /label= Glu, Gln

FT Misc-difference 9 /label= Phe, Met, Leu, His, Val

XX PN WO200207748-A2.

XX

PI Stiernberg J, Bergmann J;
 XX WPI: 2003-721552/6B.
 XX Stimulation of bone growth and cartilage formation in e.g. bone graft and
 XX arthritic joints involves administration of a thrombin derivative
 PT peptide.
 PT Disclosure; Page 8; Opp; English.

XX The sequences given in ABB80261-62 represent serine esterase conserved
 CC domains. These peptide are used as part of the thrombin peptides
 CC derivatives of the invention for stimulating bone growth. The thrombin
 CC peptide of the invention have the formula: Asp-Ala-R, where R is a
 CC serine esterase conserved domain. These peptides are used for stimulating
 CC bone growth and cartilage growth or repair in e.g. bone graft, segmental
 CC gap in a bone, bone void, at a non-union fracture, arthritic joints, and
 CC sites treated for cartilage damage or loss due to traumatic injury, and
 CC for culturing chondrocytes in vitro. The thrombin derivative peptide
 CC improves the quality of repair tissue, leads to more durable and
 CC functional restoration of joint bio mechanics, reduces the incidence of
 CC osteoarthritis in patients suffering from traumatic cartilage injuries of
 CC and accelerates the rate of normal fracture healing in fracture or small
 CC gap defects

XX Sequence 10 AA;
 SQ Query Match 78.0%; Score 46; DB 7; Length 10;
 Best Local Similarity 80.0%; Pred. No: 6 9;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CEGDGGPFV 10
 Db 1 CXDGGGKXV 10

XX Sequence 10 AA;
 SQ Query Match 72.9%; Score 43; DB 4; Length 10;
 Best Local Similarity 87.5%; Pred. No: 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CEGDGGGP 8
 Db 3 CKGDGGP 10

RESULT 8
 ID AAG94412 standard; peptide; 10 AA.
 XX
 AC AAG94412;
 AC AAG94412;
 XX DT 18-SEP-2001 (first entry)
 XX DE Human complementary peptide, SEQ ID NO: 606.
 XX KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX OS Homo sapiens.
 XX PN WO200142277-A2.
 XX PD 14-JUN-2001.
 XX PP 13-DEC-2000; 2000WO-GB004776.
 XX PR 13-DEC-1999; 99GB-00029464.
 XX PA (PROT-) PROTEOM LTD.
 XX PI Roberts GW, Heal JR;
 XX DR WPI; 2001-40819/43.
 XX Sequence 10 AA;
 SQ Query Match 70.6%; Score 34; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No: 2.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CEGDSSGG 7
 Db 2 CKGESEGG 8

The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX Example 4; Page 125, 646p; English.

XX The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification

XX Sequence 10 AA;

XX Key - Location/Qualifiers
 FH Misc-difference 2
 FT /label= Ala, Ser, Thr
 FT Misc-difference 4
 FT /label= Lys, Glu, Gln, His
 XX WO200123524-A2.
 XX (REGC) UNIV CALIFORNIA.
 XX PD 05-APR-2001.
 XX PR 02-OCT-2000; 2000WO-US027250.
 XX PR 30-SEP-1999; 99US-00410362.
 XX PA Craik CS, Takeuchi T, Shuman M;
 XX DR WPI: 2001-245002/25.
 XX N-PSDB; AAF28096.
 XX PT New nucleic acid encoding a membrane type serine protease, useful for the
 PT diagnosis, prognosis and treatment of cancer, particularly metastatic

RESULT 9
 AAJ01260
 ID AAJ01260 standard; peptide; 10 AA.
 AC AAJ01260;
 XX DT 02-JUL-2001 (first entry)
 XX DB Hepatitis C virus epitope #1251.
 XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif; antiviral.
 XX OS Hepatitis C virus.
 XX PN WO2001121189-A1.
 XX PR 29-MAR-2001.
 XX PF 19-JUL-2000; 2000WO-US019774.
 XX PR 19-JUL-1999; 99US-00357737.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT,
 DR Grey HM,
 WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus.
 PS Disclosure; Page 132; 214pp; English.
 XX The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.

Sequence 10 AA;

Query Match 52.5%; Score 31; DB 4; Length 10;
 Best Local Similarity 55.6%; Pred. No. 7.5e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 2;
 QY 2 EGDSGGPFV 10
 Db 2 KGSSGGPL 10

RESULT 10
 AAR61594
 ID AAR61594 standard; peptide; 10 AA.
 AC AAR61594;
 XX DT 25-MAR-2003 (revised)
 XX DT 12-MAY-1995 (first entry)
 DE Peptide fragment (1.0479) of HCV binds HLA-A2.1.
 XX KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV; HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; ps3; c-ERB2; Mage-1; melanoma antigen-1; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatibility complex; HLA-A2.1; gmer; 10mer; anchor; human leukocyte antigen.
 OS Hepatitis C virus.

XX PN WO9420127-A1.
 XX PD 15-SEP-1994.
 XX PF 04-MAR-1994; 94WO-US002353.
 XX PR 05-MAR-1993; 93US-00027146.
 PR 04-JUN-1993; 93US-0007305.
 PR 29-NOV-1993; 93US-00159184.
 XX PA (CYTE-) CYTEL CORP.
 XX PI Grey HM, Sette A, Sidney J, Kast W;
 XX DR WPI; 1994-302678/37.
 XX PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.
 XX PS Example 5; Page 111; 138pp; English.
 XX AAC59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (AAJ7129). AAR61594 has an IC50 of 0.0002 and the sequence occurs at position 1160 in the HCV LORF protein. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 10 AA;

Query Match 50.8%; Score 30; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EGDSGGP 8
 Db 3 KGSSGGP 9

RESULT 11

AAJ00701
 ID AAJ00701 standard; peptide; 10 AA.
 AC AAJ00701;
 XX DT 02-JUL-2001 (first entry)
 XX DE Hepatitis C virus epitope #692.
 XX XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif; antiviral.
 XX OS Hepatitis C virus.
 XX PN WO200121189-A1.
 XX PD 29-MAR-2001.
 XX PR 19-JUL-2000; 2000WO-US019774.
 XX PR 19-JUL-1999; 99US-00357737.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT,
 DR Grey HM;
 WPI; 2001-308046/32.
 XX

PT A new composition useful as a vaccines against hepatitis C virus.
 XX Disclosure; Page 117; 214pp; English.

CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention

XX Sequence 10 AA;
 SQ

Query Match 50.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1e-03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDSGGP 8
 DB 3 KGSSGGP 9

RESULT 12

AAJ01934 ID AAJ01934 standard; peptide; 10 AA.

AC AAJ01934; XX

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #11925.

KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif; antiviral.

XX Hepatitis C virus epitope #11925.

OS Hepatitis C virus.
 XX WO200121189-A1.

PR 19-JUL-1999; 99US-00357737.

(EPIM-) EPIMMUNE INC.

XX DR; 2001-308046/32.

PT A new composition useful as a vaccines against hepatitis C virus.

XX Disclosure; Page 127; 214pp; English.

CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention

XX Sequence 10 AA;

Query Match 50.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDSGGP 8
 DB 3 KGSSGGP 9

RESULT 14

AAR11746 ID AAR11746 standard; peptide; 10 AA.

AC AAR11746; XX

DT 25-MAR-2003 (revised)
 XX DT 05-JUL-1991 (first entry)

DE Cyclic platelet aggregation inhibitor - example #3.

XX Myocardial infarction; deep vein thrombosis; pulmonary embolism; stroke.
 OS Synthetic.

XX PS 214PP; English.

CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention

XX Sequence 10 AA;

Query Match 50.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDSGGP 8
 DB 3 KGSSGGP 9

XX PR 23-OCT-1999; 89US-00422906.

XX XX RESULT 13

AAJ01082 ID AAJ01082 standard; peptide; 10 AA.

PS Disclosure; Page 117; 214pp; English.

CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention

XX Sequence 10 AA;
 SQ

Query Match 50.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1e-03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDSGGP 8
 DB 3 KGSSGGP 9

RESULT 12

AAJ01934 ID AAJ01934 standard; peptide; 10 AA.

AC AAJ01934; XX

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #11925.

KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif; antiviral.

XX Hepatitis C virus epitope #11925.

OS Hepatitis C virus.
 XX WO200121189-A1.

PR 19-JUL-1999; 99US-00357737.

(EPIM-) EPIMMUNE INC.

XX DR; 2001-308046/32.

PT A new composition useful as a vaccines against hepatitis C virus.

XX Disclosure; Page 127; 214pp; English.

CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention

XX Sequence 10 AA;

Query Match 50.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDSGGP 8
 DB 3 KGSSGGP 9

RESULT 14

AAR11746 ID AAR11746 standard; peptide; 10 AA.

AC AAR11746; XX

DT 25-MAR-2003 (revised)
 XX DT 05-JUL-1991 (first entry)

DE Cyclic platelet aggregation inhibitor - example #3.

XX Myocardial infarction; deep vein thrombosis; pulmonary embolism; stroke.
 OS Synthetic.

XX PS 214PP; English.

CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention

XX Sequence 10 AA;

Query Match 50.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDSGGP 8
 DB 3 KGSSGGP 9

XX PR 23-OCT-1999; 89US-00422906.

XX XX RESULT 13

PA (SMIK) SMITHKLINE BEECHAM.
 PA (ALIF/) ALI F E.
 XX
 PI FEF, Samanen JM;
 XX
 DR; 1991-126685/18.
 XX
 New cyclic peptide(s) with Gly-Asp sequence - useful as platelet aggregation inhibitors to treat myocardial infarction, deep vein thrombosis, pulmonary embolism, stroke etc.
 XX
 Claim 9; Page 44; 55pp; English.
 XX
 The sequence is the peptide part of the cpd.: N[alpha]-Ac-cyclo(S,S)-Cys-CC Arg-Gly-Asp-Ser-Arg-Gly-Asp-Ser-Cys-NH2 See also AAR11743-R11748 for examples. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 10 AA;
 Query Match 49.2%; Score 29; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CEGDSGG 7
 Db 1 CRGDSRG 7
 Search completed: February 26, 2004, 09:21:29
 Job time : 51.5 secs

RESULT 15
 AAR11747
 ID AAR11747 standard; peptide; 10 AA.
 XX
 AC AAR11747;
 XX DT 25-MAR-2003 (revised)
 DT 05-JUL-1991 (first entry)
 XX DE Cyclic platelet aggregation inhibitor - example #4.
 XX RW Myocardial infarction; deep vein thrombosis; pulmonary embolism; stroke.
 XX OS Synthetic.
 XX EP425212-A.
 PN 02-MAY-1991.
 XX 22-OCT-1990; 90EP-00311537.
 XX PR 23-OCT-1989; 89US-00425906.
 XX PA (SMIK) SMITHKLINE BEECHAM.
 PA (ALIF/) ALI F E.
 XX
 PI FEF, Samanen JM;
 XX DR; 1991-126685/18.
 XX
 New cyclic Peptide(s) with Gly-Asp sequence - useful as platelet aggregation inhibitors to treat myocardial infarction, deep vein thrombosis, pulmonary embolism, stroke etc.
 XX
 Claim 9; Page 44; 55pp; English.
 XX
 The sequence is the peptide part of the cpd.: N[alpha]-Ac-cyclo(S,S)-Cys-CC Arg-Gly-Asp-Ser-Lys-Gly-Glu-Ser-Cys-NH2 See also AAR11743-R11748 for examples. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 10 AA;
 Query Match 49.2%; Score 29; DB 2; Length 10;

; Patent No. US20020128302A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carney, Darrell H.
 ; APPLICANT: Crowther, Roger S.
 ; APPLICANT: Simmons, David J.
 ; APPLICANT: Yang, Jiping
 ; APPLICANT: Redin, William R.
 ; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 ; FILE REFERENCE: 3033-1002-001
 ; CURRENT APPLICATION NUMBER: US/09/909,122
 ; CURRENT FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: US 60/219,300
 ; PRIOR FILING DATE: 2000-07-19
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 10
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-122-1

Query Match	100.0%	Score 59;	DB 9;	Length 10;
Best Local Similarity	100.0%	Pred. No. 0.0057;	Mismatches 0;	Indels 0;
Matches 10;	Conservative 0;	Gaps 0;		

Qy 1 CEGDGGPPV 10
 Db 1 CEGDGGPPV 10

RESULT 3

; Sequence 1, Application US/10050692
 ; GENERAL INFORMATION:
 ; APPLICANT: Carney, Darrell H.
 ; APPLICANT: Crowther, Roger S.
 ; APPLICANT: Simmons, David J.
 ; APPLICANT: Yang, Jiping
 ; APPLICANT: Redin, William R.
 ; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 ; FILE REFERENCE: 3033-1002-004
 ; CURRENT APPLICATION NUMBER: US/10/050,692
 ; CURRENT FILING DATE: 2002-01-16
 ; PRIOR APPLICATION NUMBER: US/09/909,122
 ; PRIOR FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: US 60/219,300
 ; PRIOR FILING DATE: 2000-07-19
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fragment of human prothrombin
 US-10-050-692-1

Query Match	100.0%	Score 59;	DB 13;	Length 10;
Best Local Similarity	100.0%	Pred. No. 0.0057;	Mismatches 0;	Indels 0;
Matches 10;	Conservative 0;	Gaps 0;		

Qy 1 CEGDGGPPV 10
 Db 1 CEGDGGPPV 10

RESULT 4

; Sequence 1, Application US/10050688
 ; Publication No. US20020198154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carney, Darrell H.
 ; APPLICANT: Crowther, Roger S.
 ; APPLICANT: Stieremberg, Janet
 ; APPLICANT: Bergmann, John
 ; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH ACTIVATED THROMBIN
 ; FILE REFERENCE: 3033-1003-004
 ; CURRENT APPLICATION NUMBER: US/10/050,688
 ; CURRENT FILING DATE: 2002-01-16
 ; PRIOR APPLICATION NUMBER: US/09/909,348
 ; PRIOR FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: 60/219,800
 ; PRIOR FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide fragment of thrombin
 US-10-050-688-1

Query Match	100.0%	Score 59;	DB 13;	Length 10;
Best Local Similarity	100.0%	Pred. No. 0.0057;	Mismatches 0;	Indels 0;
Matches 10;	Conservative 0;	Gaps 0;		

Qy 1 CEGDGGPPV 10
 Db 1 CEGDGGPPV 10

RESULT 5

; Sequence 2, Application US/09909348
 ; Patent No. US2002014237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carney, Darrell H.
 ; APPLICANT: Crowther, Roger S.
 ; APPLICANT: Stieremberg, Janet
 ; APPLICANT: Bergmann, John
 ; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
 ; FILE REFERENCE: 3033-1003-002
 ; CURRENT APPLICATION NUMBER: US/09/909,348
 ; CURRENT FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: US 60/219,800
 ; PRIOR FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 2
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-348-2

Query Match	100.0%	Score 59;	DB 9;	Length 10;
Best Local Similarity	100.0%	Pred. No. 0.62;	Mismatches 0;	Indels 0;
Matches 8;	Conservative 8;	Gaps 0;		

Qy 1 CEGDGGPPV 10
 Db 1 CXGDSGGPPXV 10

RESULT 6

; Sequence 1, Application US/10050688
 ; Publication No. US20020198154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carney, Darrell H.
 ; APPLICANT: Crowther, Roger S.
 ; APPLICANT: Stieremberg, Janet
 ; APPLICANT: Bergmann, John
 ; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH ACTIVATED THROMBIN
 ; FILE REFERENCE: 3033-1003-004
 ; CURRENT APPLICATION NUMBER: US/10/050,688
 ; CURRENT FILING DATE: 2002-01-16
 ; PRIOR APPLICATION NUMBER: US/09/909,122
 ; PRIOR FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: US 60/219,300
 ; PRIOR FILING DATE: 2000-07-19
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Xaa at position two is Glu or Gln
 ; NAME/KEY: VARIANT
 ; LOCATION: (1) ..(10)
 ; OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
 US-10-050-688-1

Query Match	78.0%	Score 46;	DB 9;	Length 10;
Best Local Similarity	80.0%	Pred. No. 0.62;	Mismatches 0;	Indels 2;
Matches 8;	Conservative 8;	Gaps 0;		

Qy 1 CEGDGGPPV 10
 Db 1 CXGDSGGPPXV 10

RESULT 6
US-09-909-122-2
Sequence 2, Application US/09909122
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
FILE REFERENCE: 3033.1002.001
CURRENT APPLICATION NUMBER: US/09/909.122
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Peptide fragment of Thrombin
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa at position two is Glu or Gln
OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-122-2
Query Match 78.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CEGDGGPPV 10
Db 1 CXGDSGPXV 10

RESULT 7
US-10-050-692-2
Sequence 2, Application US/10050692
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
FILE REFERENCE: 3033.1002.004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,800
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide fragment of thrombin
NAME/KEY: VARIANT
LOCATION: (2)...(2)
OTHER INFORMATION: Xaa = Glu or Gln
FEATURE:
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-2
Query Match 78.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CEGDGGPPV 10
Db 1 CXGDSGPXV 10

RESULT 9
US-09-572-404B-606
Sequence 606, Application US/09572404B
GENERAL INFORMATION:
APPLICANT: Protein Lcd
TITLE OF INVENTION: Complementary Peptide ligands from the human genome
FILE REFERENCE: Human Patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0

SEQ ID NO 606
i LENGTH: 10
i TYPE: PRT
i ORGANISM: Homo Sapiens
i FEATURE:
i OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence US-09-572-404B-606

Query Match 57.6%; Score 34; DB 10; Length 10;
 Best Local Similarity 71.4%; Pred. No. 47;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDGGG 7
 Db 2 CKGESEGG 8

RESULT 10
 US-09-572-404B-3584
i Sequence 3584, Application US/09572404B
i Publication No. US0000078374A1
i GENERAL INFORMATION:
i APPLICANT: Proteom Ltd.
i TITLE OF INVENTION: Complementary peptide ligands from the human genome
i TITLE REFERENCE: Human Patent
i CURRENT APPLICATION NUMBER: US/09/572,404B
i CURRENT FILING DATE: 2000-05-17
i NUMBER OF SEQ ID NOS: 4203
i SOFTWARE: ProtPatent version 1.0
i SEQ ID NO 3584
i LENGTH: 10
i TYPE: PRT
i ORGANISM: Homo Sapiens
i FEATURE:
i OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence US-09-572-404B-3584

Query Match 47.5%; Score 28; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GDSSCG 7
 Db 6 GDSSCG 10

RESULT 11
 US-09-572-404B-3784
i Sequence 3784, Application US/09572404B
i Publication No. US00030078374A1
i GENERAL INFORMATION:
i APPLICANT: Proteom Ltd.
i TITLE OF INVENTION: Complementary peptide ligands from the human genome
i TITLE REFERENCE: Human Patent
i CURRENT APPLICATION NUMBER: US/09/572,404B
i CURRENT FILING DATE: 2000-05-17
i NUMBER OF SEQ ID NOS: 4203
i SOFTWARE: ProtPatent version 1.0
i SEQ ID NO 3784
i LENGTH: 10
i TYPE: PRT
i ORGANISM: Homo Sapiens
i FEATURE:
i OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence US-09-572-404B-3784

Query Match 45.8%; Score 27; DB 10; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSSGGP 8
 Db 3 GASGGGP 8

RESULT 12
 US-09-572-404B-3785
i Sequence 3785, Application US/09572404B
i Publication No. US20030078374A1
i GENERAL INFORMATION:
i APPLICANT: Proteom Ltd.
i TITLE OF INVENTION: Complementary peptide ligands from the human genome
i FILE REFERENCE: Human Patent
i CURRENT APPLICATION NUMBER: US/09/572,404B
i CURRENT FILING DATE: 2000-05-17
i NUMBER OF SEQ ID NOS: 4203
i SOFTWARE: ProtPatent version 1.0
i SEQ ID NO 3785
i LENGTH: 10
i TYPE: PRT
i ORGANISM: Homo Sapiens
i FEATURE:
i OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with Sequence US-09-572-404B-3785

Query Match 45.8%; Score 27; DB 10; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSSGGP 8
 Db 3 GASGGGP 8

RESULT 13
 US-09-572-957-55
i Sequence 55, Application US/9879957
i Patent No. US002003475SA1
i GENERAL INFORMATION:
i APPLICANT: SPARKS, Andrew B.
i HOFFMAN, No.
i KAY, Brian K.
i FOWLER, Dana M.
i MCCONNELL, Stephen J.
i TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME

NUMBER OF SEQUENCES: 227
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie E Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/879,957
 FILING DATE: 13-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/630,915
 FILING DATE: 03-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 11-01-174
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDBENDS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 FEATURE: NAME/KEY Other
 LOCATION: 8
 OTHER INFORMATION: SEQ ID NO: 55;
 SEQ-DESCR: US-09-909-348-1

RESULT 14
 US-09-572-404B-51
 Sequence 51, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protpatent version 1.0
 SEQ ID NO 51
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:
 OTHER INFORMATION: sequence located in CBFA2 OR AML1 at 360-369 and may interact with
 US-09-572-404B-51

RESULT 15
 US-09-572-404B-53
 Sequence 53, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protpatent version 1.0
 SEQ ID NO 53
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:

; OTHER INFORMATION: sequence located in CBFA2 OR AML1 at 360-369 and may interact with
 ; OTHER INFORMATION: Sequence 54 in this patent.
 ; US-09-572-404B-53

Query Match 42.4%; Score 25; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 GGPF 9
 Db 7 GGPF 10

Search completed: February 26, 2004, 09:31:59
 Job time : 27.5 secs

RESULT 14
 US-09-572-404B-51
 Sequence 51, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protpatent version 1.0
 SEQ ID NO 51
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:
 OTHER INFORMATION: sequence located in CBFA2 OR AML1 at 360-369 and may interact with
 US-09-572-404B-51

RESULT 15
 US-09-572-404B-53
 Sequence 53, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd.
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protpatent version 1.0
 SEQ ID NO 53
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:19:44 ; Search time 15.5 Seconds
(without alignments) 33.307 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDGGPPV 10

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 13857

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database	Issued Patents AA: 1: /cgzn2_6/ptodata/2/iaa/5A_COMB.DEP: 2: /cgzn2_6/ptodata/2/iaa/5B_COMB.DEP: 3: /cgzn2_6/ptodata/2/iaa/6A_COMB.DEP: 4: /cgzn2_6/ptodata/2/iaa/6B_COMB.DEP: 5: /cgzn2_6/ptodata/2/iaa/PCHTUS_COMB.DEP: 6: /cgzn2_6/ptodata/2/iaa/backfile1.DEP: *	Description
1	25 42.4 10 3 US-09-010-290-6 Sequence 6, Appli	
2	25 42.4 10 4 US-09-630-915A-55 Sequence 5, Appli	
3	24 40.7 10 1 US-09-282-758B-36 Sequence 36, Appli	
4	24 40.7 10 3 US-08-159-339A-827 Sequence 827, Appli	
5	24 40.7 10 0 US-09-139-802-B8 Sequence 58, Appli	
6	24 40.7 10 4 US-09-659-786-38 Sequence 58, Appli	
7	24 40.7 10 4 US-08-407-620A-3 Sequence 3, Appli	
8	24 40.7 10 4 US-08-926-367-0 Sequence 15, Appli	
9	23 39.0 10 1 US-07-842-089E-15 Sequence 15, Appli	
10	23 39.0 10 1 US-08-264-485-15 Sequence 2, Appli	
11	23 39.0 10 0 US-08-340-428B-40 Sequence 40, Appli	
12	23 39.0 10 2 US-08-993-738A-9 Sequence 9, Appli	
13	23 39.0 10 2 US-08-361-864-36 Sequence 36, Appli	
14	23 39.0 10 0 US-09-502-367-7 Sequence 7, Appli	
15	23 39.0 10 3 US-08-535-170-9 Sequence 9, Appli	
16	23 39.0 10 3 US-08-836-786-2 Sequence 2, Appli	
17	23 39.0 10 3 US-08-713-354C-9 Sequence 9, Appli	
18	23 39.0 10 4 US-09-241-268-9 Sequence 9, Appli	
19	23 39.0 10 0 US-09-495-562-9 Sequence 6, Appli	
20	23 39.0 10 4 US-09-424-656-6 Sequence 6, Appli	
21	23 39.0 10 4 US-09-628-655-21 Sequence 21, Appli	
22	23 39.0 10 5 PCT-US93-070306-00 Sequence 40, Appli	
23	22.5 38.1 10 3 US-08-925-002-65 Sequence 65, Appli	
24	22.5 38.1 10 4 US-09-910-552-65 Sequence 65, Appli	
25	22 37.3 10 1 US-08-212-86A-3 Sequence 3, Appli	
26	22 37.3 10 1 US-08-105-222-6 Sequence 6, Appli	
27	22 37.3 10 1 US-08-425-238-2 Sequence 2, Appli	

ALIGNMENTS

RESULT 1
US-09-010-290-6
; Sequence 6, Application US/09010290
; Patent No. 6217846

GENERAL INFORMATION:

APPLICANT: Shuttle TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR USE IN THROMBUS DETECTION
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEES: Banner & Witcoff, Ltd.
STREET: 28 State St., 28th Floor
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010-290
FILING DATE: 21-JAN-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB8914020-6
FILING DATE: 19-JUN-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00933
FILING DATE: 18-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/659,343
FILING DATE: 21-MAR-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/963,127
FILING DATE: 19-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/816,922
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D. Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3998/73503
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-227-4399
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

RESULT 3
 US-08-282-758B-36
 Sequence 36, Application US/08282758B
 Patent No. 5670310

GENERAL INFORMATION:
 APPLICANT: Fields, Howard A.
 APPLICANT: Kudryakov, Yury E.
 TITLE OF INVENTION: Methods and Compositions for Differential Diagnosis of Chronic and Acute Hepatitis C
 TITLE OF INVENTION: Virus Infection
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.A.
 ZIP: 30303

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/282,758B
 FILING DATE: 29-JUL-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Jamie L.
 REGISTRATION NUMBER: 32,467
 REFERENCE/DOCKET NUMBER: 03063-0100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 818-3700
 TELEFAX: (404) 818-3799
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-282-758B-36

Query Match 40.7%; Score 24; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;

RESULT 4
 US-08-159-339A-827
 Sequence 827, Application US/08159339A
 Patent No. 603115

GENERAL INFORMATION:
 APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and Their
 FEATURES:
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834

Query Match 42.4%; Score 25; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query 1 CBGDSGG 7
 Db 1 CMGDSLG 7

COMPUTER READABLE FORM:
 MEDIUM TYPE: Disquette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lawyer
 REGISTRATION NUMBER: 32,762
 REFERENCE DOCKET NUMBER: 086223-005030US
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX:
 INFORMATION FOR SEQ ID NO: 827:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-159-339A-827

Query Match Score 24; DB 3; Length 10;

Best Local Similarity 44.4%; Pred. No. 7.6e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Query 2 EGDSGGPPV 10
 Db 1 KGEGAGAPGV 9

RESULT 5
 US-09-139-802-58
 Sequence 58, Application US/09139802
 Patent No. 6180084

GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
 TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

TITLE OF INVENTION: Same
 FILE REFERENCE: P-LJ 3203
 CURRENT APPLICATION NUMBER: US/09/139,802
 EARLIER FILING DATE: 1998-08-25

EARLIER APPLICATION NUMBER: 08/926,914
 EARLIER FILING DATE: 1997-09-10

EARLIER APPLICATION NUMBER: 08/710,067
 EARLIER FILING DATE: 1996-09-10

NUMBER OF SEQ ID NOS: 226
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 58

LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide

US-09-139-802-58
 Query Match Score 24; DB 3; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.6e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 1 CEGDSG 6
 Db 1 CEGVNG 6

RESULT 6
 US-09-659-786-58
 Sequence 58, Application US/09659786
 Patent No. 6491894

GENERAL INFORMATION:
 APPLICANT: Pasqualini, Renata
 TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
 TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

TITLE OF INVENTION: Same
 FILE REFERENCE: P-LJ 3203
 CURRENT APPLICATION NUMBER: US/09/659,786

PRIOR APPLICATION NUMBER: 08/926,914
 PRIOR FILING DATE: 1997-09-10

PRIOR APPLICATION NUMBER: 08/710,067
 PRIOR FILING DATE: 1996-09-10

NUMBER OF SEQ ID NOS: 226
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 58

LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide

US-09-659-786-58
 Query Match Score 24; DB 4; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.6e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 1 CEGDSG 6
 Db 1 CEGVNG 6

RESULT 7
 US-08-407-620A-3
 Sequence 3, Application US/08407620A
 Patent No. 6569410

GENERAL INFORMATION:
 APPLICANT: Waldmann, Herman
 APPLICANT: Clark, Michael R.
 APPLICANT: Winter, Gregory P.
 APPLICANT: Rechmann, Lutz
 TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/407,620A
 FILING DATE: 21-MAR-1995
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/235,705
 FILING DATE: 29-APR-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/099, 480
 FILING DATE: 30-JUL-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/921, 601
 FILING DATE: 03-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/424, 233
 FILING DATE: 12-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 88036228
 FILING DATE: 12-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 8804464
 FILING DATE: 25-FEB-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: MITCHARD, LEONARD C.
 REGISTRATION NUMBER: 29, 009
 REFERENCE/DOCKET NUMBER: 604-325
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 TELEX: 200/97 NIXN UR
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10
 TYPE: amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-407-620A-3

Query Match 40.7%; Score 24; DB 4; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CEGDSGG 9
 Db 1 EGHTAAFP 8

RESULT 8
 US-08-926-914-58
 Sequence 58, Application US/08926914
 Patent No. 6576239
 GENERAL INFORMATION:
 APPLICANT: Rioslantri, Renata
 APPLICANT: Pasqualini, Renata
 TITLE OF INVENTION: Tumor Honing Molecules, Conjugates
 and Methods of Using Same
 NUMBER OF SEQUENCES: 199
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/926, 914
 FILING DATE: 10-SEP-1997
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 435
 NAME: Campbell, Kathryn A.
 REGISTRATION NUMBER: 31, 815
 REFERENCE/DOCKET NUMBER: P-LJ 2725
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEX: (619) 535-8949

Query Match 39.0%; Score 23; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.1e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDSGG 7

Db |||
 2 CEMDGSG 8

RESULT 10
Sequence 15, Application US/08264485
; Pat. No. 5439820

GENERAL INFORMATION:
APPLICANT: SARMIENTOS, PABLO
DE TAXIS DU POET, PHILIPPE

APPLICANT: NITTI, GIAMBALO
APPLICANT: SCACHELLI, EMANUELA

TITLE OF INVENTION: ANTI-THROMBIN POLYPEPTIDES
NUMBER OF SEQUENCE: 59

CORRESPONDENCE ADDRESS:
OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,485

FILING DATE: 23-JUN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,089
FILING DATE: 26-FEB-1992

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5439820man F.

REGISTRATION NUMBER: 24,678
REFERENCE/DOCKET NUMBER: 769-265-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-1000

TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Hirudinaria manillensis

FEATURE: Region
NAME/KEY: Region
LOCATION: 1..10
OTHER INFORMATION: /note= "This sequence corresponds to amino acids 27-36 of SEQ ID NO:1."

US-08-264-485-15
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Hirudinaria manillensis

FEATURE: Region
NAME/KEY: Region
LOCATION: 1..10
OTHER INFORMATION: /note= "This sequence corresponds to amino acids 27-36 of SEQ ID NO:1."

US-08-264-485-15
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Hirudinaria manillensis

Db |||
 2 CEMDGSG 8

RESULT 11
US-08-340-428B-40
Sequence 40, Application US/08340428B
Patent No. 5618465
GENERAL INFORMATION:

APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renée K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brody and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 Nov. 564845ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brody, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-638-3528
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-340-428B-40

Query Match 39.0% Score 23; DB 1; Length 10;
Best Local Similarity 66.7% Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GDSGGP 8
Db 3 GDGATP 8

RESULT 12
US-08-993-738A-9
Sequence 9, Application US/08993738A
; Patent No. 592938
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;
; APPLICANT: Boon-Palleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Comprise With
; HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/993,738A
 FILING DATE: 19-December-1997
 CLASSIFICATION: 536
 PRIORITY INFORMATION:
 REFERENCE/DOCKET NUMBER: US/08/909-348-1
 APPLICATION NUMBER: 08/713,354
 FILING DATE: 13-September-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, NO. 5928938man D.
 REGISTRATION NUMBER: 30,946
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-3884
 TELEFAX: (212) 638-3884
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-993-738A-9

Qy	5 SGGP 8	Query Match	39.0%	Score 23;	DB 2;	Length 10;
Db	3 SGGP 6	Best Local Similarity	100.0%	Pred. No. 1.1e+03;	80.0%	
		Matches	4;	Conservative	0;	Mismatches
				Indels	0;	Gaps

RESULT 13
 US-08-361-864-16
 Sequence 36, Application US/08361864
 Patent No. 597064
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 ATTORNEY: Lister-James, John
 TITLE OF INVENTION: Multimeric Polyvalent Antithrombotic
 NUMBER OF SEQUENCES: 37
 TITLE OF INVENTION: Agents
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Allegretti & Witcoff, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/361,864
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/955,466A
 FILING DATE: 19-92-0002
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5977064man, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,668
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 910-221-5317
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 FEATURE: Modified-site
 NAME/KEY: Modified-site
 LOCATION: 1..5
 OTHER INFORMATION: /label= Cyclic
 /note= "The sidechain sulfur of the 1st cysteine
 is protected by an -CH2O- group, that also forms
 an amide bond with the N-terminus; the Y is the D
 atom
 ATTORNEY/AGENT INFORMATION:
 NAME/KEY: Modified-site
 LOCATION: 6..8
 OTHER INFORMATION: /label= Tc-99m-binding
 /note= "The sidechain sulfur atom of each cysteine
 is protected by an acetamido group; the C-terminal
 cysteine is an amide"
 OTHER INFORMATION: US-08-361-864-36

Qy	3 GDSGG 7	Query Match	39.0%	Score 23;	DB 2;	Length 10;
Db	3 GDCGG 7	Best Local Similarity	80.0%	Pred. No. 1.1e+03;	80.0%	
		Matches	4;	Conservative	0;	Mismatches
				Indels	0;	Gaps

RESULT 14
 US-08-302-367-7
 Sequence 7, Application US/08902367
 Patent No. 597845
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 ATTORNEY: Lister-James, John
 TITLE OF INVENTION: Radiolabeled Compounds for Thrombus
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boehm Hulbert & Bergoff
 STREET: 300 South Wacker Drive Seventh Floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/902,367
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,668
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5977064man, Kevin E
 REGISTRATION NUMBER: 35,303
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312 913 0001
 TELEFAX: 312 913 0002
 TELEX:
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..3

OTHER INFORMATION: /label= D-Tyr
 OTHER INFORMATION: /note= "The tyrosine residue is in the D-stereochemical configuration"
 FEATURE: Modified-site
 NAME/KEY: Modified-site
 LOCATION: 1..5
 OTHER INFORMATION: /label= Cyclic
 OTHER INFORMATION: /note= "The sidechain sulfur of the Cys residue is covalently linked to the amino terminus by a -CH₂CO- group."
 OTHER INFORMATION: Terminus by a -CH₂CO- group."
 NAME/KEY: Modified-site
 LOCATION: 8..10
 OTHER INFORMATION: /label= Tc-99m-chelator
 OTHER INFORMATION: /note= "The sidechain sulfur atoms of both Cys residues are each protected with an acetamidomethyl group"
 OTHER INFORMATION: acetamidomethyl group"
 FEATURE: Modified-site
 NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: /label= Amide
 OTHER INFORMATION: /note= "The carboxyl terminus is modified to an amide"
 OTHER INFORMATION: US-08-902-377-7

Query Match Score 23; DB 2; Length 10;
 Best Local Similarity 80.0%; Prod. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDGG 7
 Db 3 GDCGG 7

RESULT 15
 US-08-335-170-9
 Sequence 9, Application US/08535170
 Patent No. 605640

GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: Lister-Jones, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: Radio-labeled Compounds for Thrombus Imaging
 TITLE OF INVENTION: Imaging
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: McDonnell Boehnen Hulbert & Berghoff
 STREET: 300 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/0B/535,170
 FILING DATE: 11-JAN-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 605640nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 90,1104-KK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312 913 0001
 TELEX: 312 913 0002

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 26, 2004, 09:17:19 ; Search time 13.5 Seconds
 (without alignments)
 71.253 Million cell updates/sec

Title: US-09-909-348-2
 Perfect score: 50
 Sequence: 1 CXGDSGGPXY 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Scoring table: 283366 seqs, 96191526 residues

Searched:
 Total number of hits satisfying chosen parameters: 311

Minimum DB seq length: 10
 Maximum DB seq length: 10

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR_78;*
 1: Pir1;*
 2: Pir2;*
 3: Pir3;*
 4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	42.0	10	PH0925	T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)
2	20	40.0	10	PH0944	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
3	18	36.0	10	C39572	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
4	18	36.0	10	B60599	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
5	17	34.0	10	D60327	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
6	17	34.0	10	XGRHE	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
7	17	34.0	10	PT0632	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
8	17	34.0	10	PT0664	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
9	17	34.0	10	PH0927	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
10	16	32.0	10	1 XASNFC	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
11	16	32.0	10	PT0676	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
12	16	32.0	10	B39572	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
13	16	32.0	10	PT0215	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
14	16	32.0	10	PH0910	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
15	16	32.0	10	D60589	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
16	16	32.0	10	E60389	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
17	16	32.0	10	AG0588	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
18	16	32.0	10	PT0243	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
19	16	32.0	10	PT0215	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
20	15	30.0	10	1 ECLQIM	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
21	15	30.0	10	1 I60588	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
22	15	30.0	10	2 PH134	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
23	15	30.0	10	2 S23371	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
24	14	28.0	10	2 F60527	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
25	14	28.0	10	2 PT0084	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
26	14	28.0	10	2 B56689	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
27	14	28.0	10	2 PK0060	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
28	14	28.0	10	2 A32195	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
29	13	26.0	10	2 S65398	T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

RESULT 3

30	13	26.0	10	2 C45474	thrombospondin 2 - ornithine decarbox
31	13	26.0	10	2 B33710	sperm-activating p
32	13	26.0	10	2 H60787	sperm-activating p
33	13	26.0	10	2 B60788	sperm-activating p
34	13	26.0	10	2 C60788	sperm-activating p
35	13	26.0	10	2 D60787	sperm-activating p
36	13	26.0	10	2 D60787	sperm-activating p
37	13	26.0	10	2 A60787	sperm-activating p
38	13	26.0	10	2 B60787	sperm-activating p
39	13	26.0	10	2 A60788	sperm-activating p
40	13	26.0	10	2 A60527	sperm-activating p
41	13	26.0	10	2 G60527	sperm-activating p
42	13	26.0	10	2 B60527	sperm-activating p
43	13	26.0	10	2 C60527	sperm-activating p
44	13	26.0	10	2 G60527	sperm-activating p
45	13	26.0	10	2 C60589	sperm-activating p

ALIGNMENTS

RESULT 1					
PH0925 T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)					
C;Species: Rattus norvegicus (Norway rat)					
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997					
C;Accession: PH0925 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vanderbark, A.A.; Wilson, D.B. J;Exp. Med.: 174, 1467-1476, 1991 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic A;Reference number: PH0891; MUID:92078857; PMID:1833012 A;Accession: PH0925 A;Molecule type: mRNA A;Residues: 1-10 <COL> A;Experimental source: concanavalin A-activated lymphoblast C;Keywords: T-cell receptor					

Query Match	42.0%	Score 21;	DB 2;	Length 10;
Best Local Similarity	42.9%	Pred. No.	8 8e+02;	
Matches	3;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;

Qy	1 CXGDGG 7	
Db	1 CASSDGG 7	

RESULT 2					
PH0944 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)					
C;Species: Rattus norvegicus (Norway rat)					
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997					
C;Accession: PH0944 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vanderbark, A.A.; Wilson, D.B. J;Exp. Med.: 174, 1467-1476, 1991 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic A;Reference number: PH0891; MUID:92078857; PMID:1833012 A;Accession: PH0944 A;Molecule type: mRNA A;Residues: 1-10 <COL> A;Experimental source: complete Freund's adjuvant-immunized lymph node A;Note: the authors translated the codon GAC for residue 9 as Glu C;Keywords: T-cell receptor					

Query Match	40.0%	Score 20;	DB 2;	Length 10;
Best Local Similarity	42.9%	Pred. No.	1.3e+03;	
Matches	3;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;

Qy	1 CXGDGG 7	
Db	1 CASSDGG 7	

C39572 is sperm-activating peptide TG-3 - sea urchin (*Tripectenustes gratilla*)
 N:Alternative names: speract homolog TG-3
 C:Species: *Tripectenustes gratilla*
 C:Accession: C39572
 C:Title: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000
 C:Accession: C39572
 C:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
 A:Reference number: A35572; MUID:91283461; PMID:2055627
 A:Accession: C39572
 A:Molecule type: Protein
 A:Residues: 1-10 <YOS>
 C:Superfamily: unassigned animal peptides
 C:Keywords: bromine
 F:Modified site: 2' -bromophenylalanine (Phe) #status experimental
 Query Match 36.0% Score 18/ DB 2; Length 10;
 Best Local Similarity 75.0% Pred. No. 3.1e+03 ;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 DSGGG 7
 | | |
 5 DGGG 8
 Db

RESULT 4
 B60589 sperm-activating peptide (Gly-3, Ser-5, Ile-9 SAP-I) - slate-pencil urchin (Heterocentrotus mamillatus)
 C:Species: Heterocentrotus mamillatus
 C:Accession: B60589
 C:Title: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 R:Yoshino, K.I.; Kajura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptide nudus. Echinometra mathiae and Heterocentrotus mammillatus.
 A:Reference number: A60527
 A:Accession: B60589
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 C:Superfamily: unassigned animal peptides
 Query Match 36.0% Score 18/ DB 2; Length 10;
 Best Local Similarity 80.0% Pred. No. 3.1e+03 ;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 GDSGG 7
 | | |
 3 GSGG 7
 Db

RESULT 5
 D60527 sperm-activating peptide (Gly-5 SAP-I) - sea urchin (*Tripectenustes gratilla*)
 N:Alternative name: speract homolog TG-6
 C:Species: *Tripectenustes gratilla*
 C:Accession: D60527; F39572
 C:Title: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 R:Yoshino, K.I.; Kajura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptide nudus. Echinometra mathiae and Heterocentrotus mammillatus.
 A:Reference number: A60527
 A:Accession: D60527
 A:Molecule type: Protein
 A:Residues: 1-10 <YOS>
 A:Note: this peptide did not contain bromophenylalanine
 R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Yamaguchi, Comp. Biochemistry 30, 6203-6209, 1991
 A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
 A:Reference number: A35572; MUID:91283461; PMID:2055627
 A:Accession: F39572
 A:Molecule type: protein

C:/Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text change 30-May-1997

RESULT 11
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PR0664
 C;Species: Anthocidaris crassispina
 C;Alternate name: Anthocidaris crassispina
 C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C;Accession: F60787
 R;Author: Kajiura, H.; Nomura, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
 A;Reference number: A60787; PMID:3378407
 A;Accession: F60787
 A;Molecule type: protein
 A;Residues: 1-10 <SQQ>
 C;Comment: This oligopeptide from egg jelly is one of several from this species, all of which shows some but not absolute species restriction.
 C;Superfamily: unassigned animal peptides

Query Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	32.0%	16	DB 2;	Length 10;			
Matches 3;	100.0%		Pred. No.	7e-03;	0;	0;	
Conservative 3;			Mismatches	0;	0;	0;	
Qy	5	SQQ	7				
Db	5	SQQ	7				

RESULT 12
 C;Species: Octopus norvegicus (Norway rat)
 C;Accession: PH0927
 C;Reference number: PH0927
 C;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
 encephalomyelitis
 A;Accession: PH0927
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
 encephalomyelitis
 A;Molecule type: mRNA
 A;Residues: 1-10 <GOL>
 A;Keywords: T-cell receptor

Query Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	34.0%	17	DB 2;	Length 10;			
Matches 3;	100.0%		Pred. No.	4.6e+03;	1;	0;	
Conservative 3;			Mismatches	1;	1;	0;	
Qy	3	GDSSGG	7				
Db	3	GDTPG	7				

RESULT 9
 C;Species: Octopus norvegicus (Norway rat)
 C;Accession: PH0927
 C;Reference number: PH0927
 C;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
 encephalomyelitis
 A;Accession: PH0927
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
 encephalomyelitis
 A;Molecule type: mRNA
 A;Residues: 1-10 <GOL>
 A;Keywords: T-cell receptor

Query Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	34.0%	17	DB 2;	Length 10;			
Matches 3;	100.0%		Pred. No.	4.6e+03;	1;	0;	
Conservative 3;			Mismatches	1;	1;	0;	
Qy	3	GDSSGG	7				
Db	3	GDTPG	7				

RESULT 13
 C;Species: Echinometra mathaei
 C;Alternate name: Echinometra mathaei
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: F60589
 R;Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related peptide
 ors from Echinometra mathaei and Heterosentrotus mammillatus.
 A;Reference number: A60527
 A;Accession: F60589
 A;Molecule type: protein
 A;Residues: 1-10 <YOS>
 C;Superfamily: unassigned animal peptides

Query Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	32.0%	16	DB 2;	Length 10;			
Matches 3;	100.0%		Pred. No.	7e-03;	0;	0;	
Conservative 3;			Mismatches	0;	0;	0;	
Qy	5	SGGP	8				
Db	5	SAGP	7				

RESULT 10
 C;Species: Vipera aspis (aspic viper)
 C;Accession: A60377
 C;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the
 Int. J. Biochem. 22, 767-771, 1990
 A;Accession: A60377
 A;Molecule type: protein
 A;Residues: 1-10 <KOM>
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid (Gln) #status experimental
 F1;Modified site: pyroglutamic acid (Gln) #status experimental

Query Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	32.0%	16	DB 1;	Length 10;			
Matches 3;	100.0%		Pred. No.	7e+03;	1;	0;	
Conservative 3;			Mismatches	0;	0;	0;	
Qy	7	GPXV	10				
Db	5	GPKV	8				

Qy 5 SGG 7
 Qy |||
 Db 5 SGG 7

RESULT 14
 D60589
 sperm-activating peptide (Ser-3,5 SAP-I) - Echinometra mathaei
 C;Species: Echinometra mathaei
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: D60589
 R;Yoshino, K.I.;Kajura, H.;Nomura, K.;Takao, T.;Shimonishi, Y.;Kurita, M.;Yamaguchi, Comp. Biochem. Physiol. B 94, 739-751, 1989
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related peptide nucleus, Echinometra mathaei and Heterocentrotus mammillatus.
 A;Reference number: A60527
 A;Accession: D60589
 A;Molecule type: protein
 A;Residues: 1-10 <YOS>
 A;Note: an identical peptide was isolated from Echinometra mathaei type A and type B
 C;Superfamily: unassigned animal peptides

Query Match Score 32.0%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No 7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SGG 7
 Qy |||
 Db 5 SGG 7

RESULT 15
 D60589
 sperm-activating peptide (Tyr-2, Ser-3,5, Ala-8, Asp-10 SAP-I) - Echinometra mathaei
 C;Species: Echinometra mathaei
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: D60589
 R;Yoshino, K.I.;Kajura, H.;Nomura, K.;Takao, T.;Shimonishi, Y.;Kurita, M.;Yamaguchi, Comp. Biochem. Physiol. B 94, 739-751, 1989
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related peptide nucleus, Echinometra mathaei and Heterocentrotus mammillatus.
 A;Reference number: A60527
 A;Accession: D60589
 A;Molecule type: protein
 A;Residues: 1-10 <YOS>
 A;Note: an identical peptide was isolated from Echinometra mathaei type A and type B
 C;Superfamily: unassigned animal peptides

Query Match Score 32.0%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No 7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SGG 7
 Qy |||
 Db 5 SGG 7

Search completed: February 26, 2004, 09:24:05
 Job time : 13.5 secs

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OM protein - protein search, using sw mode

Run on: February 26, 2004, 09:02:09 ; Search time 10.5 Seconds
(without alignments)
49.591 Million cell updates/sec

Title: US-09-909-348-2
Perfect score: 50
Sequence: 1 CXGDSGGPXPV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	17	34.0	10	1	GLEM_HUMAN	P02728	homo sapien
2	16	32.0	10	1	BPP_VIPAS	P31351	vipera aspis
3	16	32.0	10	1	ESTA_SCIGA	P81012	schizaphis
4	15	30.0	10	1	COKO_RABIT	P80335	oryctolagus
5	14	28.0	10	1	FAR6_PANRE	P82660	panagelius
6	14	28.0	10	1	TRPB_LEIMA	P81740	leucophaea
7	13	26.0	10	1	COKO RAT	P80432	rattus norvegicus
8	13	26.0	10	1	COKO THROB	P80982	thomomys obesus
9	13	26.0	10	1	PNEU_HUMAN	P22103	homo sapien
10	13	26.0	10	1	PNEU RAT	P21996	rattus norvegicus
11	12	24.0	10	1	TAKS2_AEDAE	P42635	aedes aegypti
12	12	24.0	10	1	COKH_ONCNY	P80331	oncorhynchus
13	12	24.0	10	1	CU30_LOCMI	P11735	locusta migratoria
14	12	24.0	10	1	FAR7_MACRS	P83280	macrobrachium
15	12	24.0	10	1	FARP_MYTED	P42560	mytilus edulis
16	12	24.0	10	1	TAKS1_AEDAE	P42634	aedes aegypti
17	12	24.0	10	1	TPIS_NICPL	P19118	nicociana
18	12	24.0	10	1	UPA8_HUMAN	P30094	homo sapien
19	10	20.0	10	1	CATB_SHEEP	P83205	ovis aries
20	10	20.0	10	1	PARP_LOCMI	P38553	locusta migratoria
21	10	20.0	10	1	GAJU_HUMAN	P21358	homo sapien
22	10	20.0	10	1	GON1_CLUPA	P81749	clupia pallida
23	10	20.0	10	1	HTP_HELZE	P26353	heliothis zea
24	10	20.0	10	1	LSK2_LEIMA	P09039	leucophaea
25	10	20.0	10	1	MOSQ_CLYJUA	P19962	clypeaster
26	10	20.0	10	1	NS1_MYCTU	P81135	mycobacterium
27	10	20.0	10	1	PVK_LOCMI	P83382	locusta migratoria
28	10	20.0	10	1	RPL_PHODV	P35946	photinus diabolus
29	10	20.0	10	1	SLAP_BACTV	P43325	bacillus thuringiensis
30	10	20.0	10	1	TKL2_LOCMI	P12224	locusta migratoria
31	10	20.0	10	1	TKNB_CHICK	P19851	gallus gallus
32	10	20.0	10	1	TKNB_RANCA	P26689	rana catesbeiana
33	10	20.0	10	1	TKNB_RANRI	P29135	rana ridibunda

ALIGNMENTS

P19225	aedes aegyp	34	10	20.0	TM0F_AEDAE	34	10	20.0	10	1
P81739	leucophaea	35	10	20.0	TRP7_LEIMA	35	10	20.0	10	1
P5673	ractus norv	36	10	20.0	UH05 RAT	36	10	20.0	10	1
UHA3	HUMAN	37	10	20.0	UHAS_HUMAN	37	10	20.0	10	1
UPAS5	HUMAN	38	10	20.0	URE3_HUMAN	38	10	20.0	10	1
P30091	homo sapien	39	10	20.0	URB3_HUMAN	39	10	20.0	10	1
P17339	morganella	40	9	18.0	BPP2_BOTTIN	40	9	18.0	10	1
P04930	bacillus	41	9	18.0	BPP3_BOTTIN	41	9	18.0	10	1
P30426	bacillus	42	9	18.0	BPP8_BOTTIN	42	9	18.0	10	1
P80678	chelyosoma	43	9	18.0	GON2_CHEPR	43	9	18.0	10	1
P81863	pardachirus	44	9	18.0	PAP1_PARMA	44	9	18.0	10	1
P80525	fasciola he	45	9	18.0	PCK_FASHE	45	9	18.0	10	1

RESULT 1

GI EM_HUMAN	STANDARD;	PRT;	10 AA.
ID P02758;	DT 21-JUL-1986 (Rel. 01, Created)	DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	DE Erythrocyte membrane Glycoprotein	OS Homo sapiens (Human)	
RT "New low molecular weight Glycoprotein containing triglucosylcysteine in human erythrocyte membrane."	RL Nature New Biol. 234:25-26(1971).	CC PTM: S-linked Glycan consists of GLC-GLC-GLC trisaccharide.	
CC :- MISCELLANEOUS: The identity of the Glycoprotein from which this peptide is derived is unknown. No physiological function has been attributed.	CC DR A03187: XGHIEB.	CC PIR: A03187: XGHIEB.	
CC KW Glycoprotein; Erythrocyte.	FT CARBOHYDRT	FT SEQUENCE	
CC 1	1	10 AA;	10 AA;
CC 2399FEEEA1FS1E8 CRC64;	CC MW: 1049	CC Score: 17;	CC Length: 10;
CC	CC Best Local Similarity: 60.0%;	CC Pred.: No. 1.e+03/	CC Indels: 0; Gaps: 0;
CC Matches: 3; Conservative: 0; Mismatches: 2;	CC OY 1 CXGDS 5	CC Db 1 CEGHS 5	
CC	CC DE Bradkinin-potentiating Peptide (Angiotensin-converting enzyme inhibitor).	CC OS Vipera aspis (Aspic viper)	
CC AC P31351	CC DT 01-JUL-1993 (Rel. 26, Created)	CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; Lepidosaurs; Squamata; Serpentes; Colubroidea;	
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)	CC DT 28-FEB-2003 (Rel. 41, Last annotation update)	CC OC Viperidae; Viperinae; Vipera.	
CC DE	CC RN NCBI_TaxID:8706;	CC RA Komori Y., Sugihara H.;	
CC	CC [1]	CC SEQUENCE.	
CC	CC RC TISSUE:Venom;	CC RX MEDLINE=90382616; PubMed=2169439;	
CC	CC RA		

RT "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of *Vipera aspis aspis*.";
 RT Int. J. Biochem. 22:767-771(1990)
 RL -!- FUNCTION: This Peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.

CC DR A60377; XASNPC; Pyrrolidone carboxylic acid.
 DR KWR Hypotensive agent; Pyrrolidone carboxylic acid.
 MOD RES FT PYRROLIDONE CARBOXYLIC ACID.
 SEQUENCE SQ 10 AA; 1062 MW; 3BAB27C327686773 CRC64;

Query Match Score 16; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GPXV 10
 Db 5 GPXV 8

RESULT 3 ESTA_SCHGA STANDARD; PRT; 10 AA.

AC P1012;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 DE (Fragment).
 OS Schizaphis graminum (Aphid).
 OC Schizaphis; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidoidea;
 OC Aphidoidea; Aphelinida; Aphelinini; Schizaphis.
 OX NCBI_TaxID:13262;
 RN

RP MEDLINE:97468499; PubMed=9327586;
 RA Siegfried B.D., Ono M., Swanson J.J.;
 RT "Purification and characterization of a carboxylesterase associated with organophosphate resistance in the greenbug, *Schizaphis graminum* (Homoptera: Aphididae)." ;
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a carboxylic anion.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR InterPro_IPRO00218; Carboxylesterase_B_1; PARTIAL.
 DR PROSITE; PS00522; CARBOXYLESTERASE_B_2; PARTIAL.
 DR KW Hydrolase; Serine esterase.
 FT NON_TER 10
 SEQUENCE 10 AA; 1025 MW; 018ABE5B7865A2CO CRC64;

Query Match Score 16; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SGG 7
 Db 5 SGG 7

RESULT 4 COXQ_RABBIT STANDARD; PRT; 10 AA.

AC P80316;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
 DE (Fragment).
 DE COXQR.

Query Match Score 16; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.9e-03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SGCP 8
 Db 2 SGCP 5

RESULT 5 FAR6_PANRE STANDARD; PRT; 10 AA.

AC P82650;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF6 (NGAPQQFVRF-amide).
 OS Pancrellus redivirinus.
 CC Eukaryota; Metazoa; Chromalveolida; Rhabditida;
 CC Panzerolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID:6233;

RN [1] SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RA "Isolation, characterization and pharmacology of FMRFamide-related peptides (FARPs) from free-living nematode, *Panagrellus redivirinus*."
 RA Submitted (JUL-2000) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive.
 CC -!- SIMILARITY: Belongs to the FARPs (FMRFamide related peptide)
 CC family.
 CC Neuropeptide; Amidation.
 RW FT MOD RES 10
 SEQUENCE 10 AA; 1132 MW; CB13B49CD776C76D CRC64;

Query Match Score 14; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.9e-03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SGCP 8
 Db 1 NGAP 4

RESULT 6 TRPB_LBUMA STANDARD; PRT; 10 AA.

AC P81740;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tachykinin-related peptide B (LeuTrP B).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OS Oryctolagus cuniculus (Rabbit); Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metacora; Chordata; Lagomorpha; Leporidae; Oryctolagus.
 CC NCBI_TaxID:9986;
 RN RP
 SEQUENCE.
 CC TISSUE-Heart, and Liver;
 RC Preundi R., Kadenbach B.;
 RA Submitted (MAR-1994) to Swiss-Prot.
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
 RW Oxidoreductase; Mitochondrion.
 FT NON_TER 10
 SEQUENCE 10 AA; 1027 MW; 2G325CB40DC76338 CRC64;

Query Match Score 15; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SGCP 8
 Db 2 SGCP 5

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaeia.
 OC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE: Brain;
 RX MEDLINE=97259266; PubMed=9114447;
 RA Muren J.E.; Naeffel D.R.;
 RT "Seven tachykinin-related peptides isolated from the brain of the madeira cockroach: evidence for tissue-specific expression of isoforms."
 RT Peptides 18:7-15 (1997).
 CC -!- FUNCTION: Myoactive peptide. Increases the amplitude and frequency of spontaneous contractions and tonus of hindgut muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- MASS SPECTROMETRY: MW=1076.9; METHOD=MALDI.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1076 MW;

Query Match	28.0%;	Score 14;	DB 1;	Length 10;
Best Local Similarity	50.0%;	Pred. No.	4.9e+03;	
Matches	1;	Mismatches	1;	Indels 0;
		Gaps 0;		

Qy 7 GPSV 10
 Db 1 GPSM 4

RESULT 7
 COXO_RAT
 ID COXO_RAT
 AC P80932;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1) (VIIIA) (Fragment).
 GN COXTC OR COX7C1.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=STAR; TISSUE=Heart, and Liver;
 RX MEDLINE=95124529; PubMed=7601105;
 RA Schaeffer H.; Noack H.; Halangk W.; Brandt U.; von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isozyme."
 RT Eur. J. Biochem. 230:235-241(1995).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyanocytchrome c + O₂ = 4 ferricytochrome c + 2 H⁽²⁾O.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIc family.

Query Match	26.0%;	Score 13;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No.	7.4e+03;	
Matches	2;	Mismatches	0;	Indels 0;
		Gaps 0;		

Qy 7 GP 8
 Db 6 GP 7

RESULT 8
 COXO_THUOB
 ID COXO_THUOB
 AC P80932;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIc (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Actinopterygii; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OC NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart, and Liver;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S.; Lee I.; Kim M.; Song E.; Linder D.; Lottspeich F.; Kadenbach B.; RT "The subunit structure of cytochrome c oxidase from tuna heart and liver." Eur. J. Biochem. 248:99-1103 (1997).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport. The subunit structure of cytochrome c oxidase from tuna heart and liver.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyanocytchrome c + O₂ = 4 ferricytochrome c + 2 H⁽²⁾O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 DR PIR: S77390; S77390
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCC CRC64;

Query Match	26.0%;	Score 13;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No.	7.4e+03;	
Matches	2;	Conservative	0;	Mismatches 0;
		Indels 0;		Gaps 0;

Qy 7 GP 8
 Db 6 GP 7

RESULT 9
 PNEU_HUMAN
 ID PNEU_HUMAN
 AC P22103;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pneumadin (PNN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarinini; Homidae; Homo.
 OC NCBI_TaxID=96006;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=91110910; PubMed=2274681;
 RA Batra V.K.; Mathur M.; Mir S.A.; Kapoor R.; Kumar M.A.; RT "Pneumadin: a new lung peptide which triggers anti-diuresis.";
 RT Regul. Pept. 30:77-87 (1990).
 CC -!- FUNCTION: Anti-diuretic peptide that triggers the release of ADH.
 DR PIR: B33443; B33443.
 KW Amidation.
 FT MOD RES 10
 SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match	26.0%;	Score 13;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No.	7.4e+03;	
Matches	2;	Conservative	0;	Mismatches 0;
		Indels 0;		Gaps 0;

Qy 7 GP 8
 Db 6 GP 7

FT NON_TER 10 10 AA; 969 MW; 4973E36B58772877 CRC64;
 SQ SEQUENCE 10 AA; 969 MW; 4973E36B58772877 CRC64;
 Query Match 24.0%; Score 12; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GG 7
 |
 Db 8 GG 9

RESULT 14
 FARP_MACRS STANDARD; PRT; 10 AA.
 ID FARP_MACRS
 AC P83280-
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 D3 FMRFamide-like neuropeptid ELP7 (GKDPNLFamide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Bivaliostreata; Pueraria; Decapoda; Pleocyemata; Caridea;
 OC Palaeonotoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID:79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21107394; PubMed=11179812;
 RA Sithongrungl P.; Sarithongkum W.; Longrant S.; Panchan N.;
 RA Sithongrungl W.; Petson A.;
 RT "Three more novel FMRFamide-like neuropeptide sequences from the eye stalk of the giant freshwater prawn Macrobrachium rosenbergii.";
 RL Peptides 22:191-197 (2001).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 CC GO:GO:0007218; P:neuropeptide signaling pathway; IDA.
 DR Neuropeptide; Amidation.
 PT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 124 MW; 3CFE9C9C4540AA8 CRC64;
 Query Match 24.0%; Score 12; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4
 Db 3 GD 4

FT MOD_RES 10 10 AA; 1180 MW; 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1180 MW; C2F80C9C1EAA87D CRC64;
 Query Match 24.0%; Score 12; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GD 4
 Db 4 GD 5

Search completed: February 26, 2004, 09:22:04
 Job time : 10.5 secs

RESULT 15
 FARP_MYTID STANDARD; PRT; 10 AA.
 ID FARP_MYTID
 AC P42560;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 D3 FMRFamide-like neuropeptide ALGDPHFFRF-amide.
 OS Mytilus edulis (Blue mussel).
 OC Bivalvia; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytilioida;
 OC Mytilioidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN SEQUENCE
 RP MEDLINE=93047883; PubMed=1358534;
 RA Walker R.J.;
 RA "Neuroactive peptides with an RFamide or Pamide carboxyl terminal.";
 RL Comp. Biochem. Physiol. 102C:21-22(1992).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 DR PIR; A58365; A58365.
 KW Neuropeptide; Amidation.

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:16:49 ; Search time 35 Seconds

90.148 Million cell updates/sec
(without alignments)

Title: US-09-909-348-2

Perfect score: 50

Sequence: 1 CXGDSGGPXY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31551802 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRNBL_25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_rodent:*
- 13: sp_virus:*
- 14: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archeap:*

Database :

SPTRNBL_25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_plage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_rodent:*

13: sp_virus:*

14: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archeap:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description

Query	Match	Length	DB	ID	Description
Q9TS42	Q9TS42	6	SPTRNBL_25	Q9TS42	Q9TS42 sus scrofa
P82938	P82938	10	SPTRNBL_25	P82938 hordeum vulgare	
Q9533	Q9533	2	SPTRNBL_25	Q9533 escherichia coli	
Q9x34	Q9x34	2	SPTRNBL_25	Q9x34 leclercia australis	
Q9nf2	Q9nf2	2	SPTRNBL_25	Q9nf2 homo sapiens	
Q9ub86	Q9ub86	4	SPTRNBL_25	Q9ub86 homo sapiens	
Q947R7	Q947R7	7	SPTRNBL_25	Q947R7 solanum tuberosum	
Q9ney9	Q9ney9	10	SPTRNBL_25	Q9ney9 homo sapiens	
P82222	P82222	10	SPTRNBL_25	P82222 bombyx mori	
Q9t33	Q9t33	11	SPTRNBL_25	Q9t33 canis familiaris	
Q9avk7	Q9avk7	11	SPTRNBL_25	Q9avk7 mus musculus	
Q96oA7	Q96oA7	12	SPTRNBL_25	Q96oA7 homo sapiens	
Q9P229	Q9P229	13	SPTRNBL_25	Q9P229 homo sapiens	
Q9S936	Q9S936	13	SPTRNBL_25	Q9S936 beta vulgaris	
Q9QVF0	Q9QVF0	14	SPTRNBL_25	Q9QVF0 mus musculus	
Q9QVE9	Q9QVE9	15	SPTRNBL_25	Q9QVE9 mus musculus	

050032 mycobacteri	17	28.0	10	2	050032	
Q9bj78 bos mutus	18	14	10	6	Q8M778	
Q9prspars aura	19	14	10	2	Q9PRU9	
Q9tf1 pseudomonas	20	13	26.0	10	2	Q9RTJ1
Q93im2 prochlorococcus	21	13	26.0	10	2	Q9XIM2
Q977j felicibacter	22	13	26.0	10	4	Q9R7J8
Q8za2 homo sapien	23	13	26.0	10	4	Q8IZA2
Q8bh93 brookesia	24	13	26.0	10	8	Q8SH93
Q8az9 pyrrhobryum	25	13	26.0	10	8	Q8AZ9
Q99213 aegilops	26	13	26.0	10	10	Q99213
Q9yoro brassica	27	13	26.0	10	10	Q7YORO
Q93389 rattus norvegicus	28	13	26.0	10	11	Q63389
Q93978 influenzae	29	13	26.0	10	12	Q83978
P90373 suis herpes	30	13	26.0	10	13	P90373
Q0oy93 gallus gallus	31	13	26.0	10	13	Q3594
Q98d29 trypanosoma	32	13	26.0	10	13	Q86D29
Q8Bpn8 macaca mulatta	33	12	24.0	10	10	Q8BPN8
Q86622 rattus norvegicus	34	12	24.0	10	6	Q8SPNB
P82223 bombyx mori	35	12	24.0	10	2	P51812
P82224 bombyx mori	36	12	24.0	10	4	P0493
Q9ucu6 homo sapiens	37	12	24.0	10	4	Q9UCU6
Q725A2 homo sapiens	38	12	24.0	10	4	Q725A2
Q86D29	39	12	24.0	10	5	Q86D29
Q8Bpn8 macaca mulatta	40	12	24.0	10	6	Q8BPN8
Q86622 rattus norvegicus	41	12	24.0	10	11	Q86622
P82223 bombyx mori	42	11	22.0	10	5	P82223
P82224 bombyx mori	43	11	22.0	10	5	P82224
Q8wp04 atelus belzunces	44	11	22.0	10	6	Q8WP04
Q9Tr48 bos taurus	45	11	22.0	10	6	Q9TR48

ALIGNMENTS

RESULT 1	Q9TS42	PRELIMINARY;	PRT;	PRT;	PRT;
AC	Q9TS42;	AC	Q9TS42;	AC	Q9TS42;
DT	01-MAY-2000	DT	01-MAY-2000	DT	01-MAY-2000
DT	(TRIMBLrel. 13, Created)	DT	(TRIMBLrel. 13, Last sequence update)	DT	(TRIMBLrel. 21, Last annotation update)
DT	01-JUN-2002	DT	01-JUN-2002	DT	01-JUN-2002
DE	OESTRADIOL-RECEPTOR-P2 peptide (fragment).	DE	OESTRADIOL-RECEPTOR-P2 peptide (fragment).	DE	OESTRADIOL-RECEPTOR-P2 peptide (fragment).
OS	Sus scrofa (Pig).	OS	Bukarota; Metzaot; Chordata; Crustacea; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.	OS	Bukarota; Metzaot; Chordata; Crustacea; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX	NCBI_TaxID=9822;	OX	NCBI_TaxID=9822;	OX	NCBI_TaxID=9822;
RN	[1]	RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
PX	MEDLINE=91291128; PubMed=2064608;	PX	MEDLINE=91291128; PubMed=2064608;	PX	MEDLINE=91291128; PubMed=2064608;
RA	Thiele H.H., Jungblut P.W., Jakob F.,	RA	Thiele H.H., Jungblut P.W., Jakob F.,	RA	Thiele H.H., Jungblut P.W., Jakob F.,
RT	"The Proton-driven dissociation of oestradiol-receptor dimers as a preparative tool. Isolation of a 32 kDa fragment from Porcine uterus and assignment of C-terminal origin by partial sequencing."	RT	"The Proton-driven dissociation of oestradiol-receptor dimers as a preparative tool. Isolation of a 32 kDa fragment from Porcine uterus and assignment of C-terminal origin by partial sequencing."	RT	"The Proton-driven dissociation of oestradiol-receptor dimers as a preparative tool. Isolation of a 32 kDa fragment from Porcine uterus and assignment of C-terminal origin by partial sequencing."
RL	Biolog. J. 276:709-714 (1991).	RL	Biolog. J. 276:709-714 (1991).	RL	Biolog. J. 276:709-714 (1991).
FT	NON_TER	FT	NON_TER	FT	NON_TER
PT	1	PT	10	PT	10
SQ	992 MW;	SQ	992 MW;	SQ	992 MW;
Query	4 DSGGP 8	Query	4 DSGGP 8	Query	4 DSGGP 8
Db	6 NEGGP 10	Db	6 NEGGP 10	Db	6 NEGGP 10

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	40.0	10	6	SPTRNBL_25	Q9TS42	Q9TS42 sus scrofa
2	20	40.0	10	10	SPTRNBL_25	P82938	P82938 hordeum vulgare
3	17	34.0	10	2	SPTRNBL_25	Q9533	Q9533 escherichia coli
4	17	34.0	10	2	SPTRNBL_25	Q9x34	Q9x34 leclercia australis
5	17	34.0	10	4	SPTRNBL_25	Q9nf2	Q9nf2 homo sapiens
6	17	34.0	10	4	SPTRNBL_25	Q9ub86	Q9ub86 homo sapiens
7	17	34.0	10	10	SPTRNBL_25	Q947R7	Q947R7 solanum tuberosum
8	16	32.0	10	4	SPTRNBL_25	Q9ney9	Q9ney9 homo sapiens
9	16	32.0	10	5	SPTRNBL_25	P82222	P82222 bombyx mori
10	16	32.0	10	6	SPTRNBL_25	Q9t33	Q9t33 canis familiaris
11	16	32.0	10	11	SPTRNBL_25	Q9avk7	Q9avk7 mus musculus
12	15	30.0	10	4	SPTRNBL_25	Q96oA7	Q96oA7 homo sapiens
13	15	30.0	10	4	SPTRNBL_25	Q9P229	Q9P229 homo sapiens
14	15	30.0	10	10	SPTRNBL_25	Q9S936	Q9S936 beta vulgaris
15	15	30.0	10	11	SPTRNBL_25	Q9QVF0	Q9QVF0 mus musculus
16	15	30.0	10	11	SPTRNBL_25	Q9QVE9	Q9QVE9 prokaryotes

Query Match Length DB ID Description

Score 40.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Score 20.0%; Best Local Similarity 60.0%; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE Unknown endosperm protein C (Fragment).
OS Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Striophtyta; Embryophytia; Trachophytia;
CC Triticeae; Hordeum.
OC Poaceae; Pooideae;
.OX NCBI_TaxID=4513;

RN [1] SEQUENCE.
RX STRAIN=CV_BOM1; TISSUE=Starchy endosperm;
MEDLINE=2108891; PubMed=11271488;

RN Kristoffersen H.E., Flensrud R.;
RT "Separation and characterization of basic barley seed proteins.";
RL Electrophoresis 21:363-3700 (2000).

-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 kDa.
FT NON_TER 10 10 MW; 98562DC40AA87AAE CRC64;
SQ SEQUENCE 10 AA; 1053 MW;

Query Match Score 20%; DB 10%; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXGD 4
Db 3 CDGD 6

RESULT 4
ID Q9X534 PRELIMINARY; PRT; 10 AA.
AC Q9X534; PRELIMINARY; PRT; 10 AA.
DT 01-NOV-1999 (TREMBrel. 12, Created)
DT 01-NOV-1999 (TREMBrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Leclercia adecarboxylata.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteroidales; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
.OX NCBI_TaxID=81355;
RN SEQUENCE FROM N.A.
RP SPBATTN=742H;
RC MEDLINE=9720820; PubMed=9055422;
RX Liebert C.A., Wireman J., Smith T., Summers A.O.;
RA "Association of mercury resistance (mer) operons of Gram-negative
bacteria isolated from the fecal flora of primates.";
RT "Phylogeny of mercury resistance (mer) operons of Gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=742H;
RX MEDLINE=98027386; PubMed=9361433;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
gram-negative fecal bacteria of primates";
RL Appl. Environ. Microbiol. 63:4494-4503 (-997).
RN SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622 (2000).
DR EMBL; AF120965; AAD23785.1; -.
RN SEQUENCE FROM N.A.
RC MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of Gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=209A;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
Gram-negative fecal bacteria of primates";
RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
RN SEQUENCE FROM N.A.
RC MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622 (2000).
DR EMBL; AF120964; AAD23783.1; -.
FT NON_TER 1 1 MW; 3F526335A5A77B58 CRC64;
SQ SEQUENCE 10 AA; 1093 MW;

Query Match Score 17%; DB 2%; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DSGGP B
Db 1 DAGYP 5

RESULT 5
ID Q9UNF2 PRELIMINARY; PRT; 10 AA.
AC Q9UNF2; PRELIMINARY; PRT; 10 AA.
DT 01-MAY-2000 (TREMBrel. 13, Created)
DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)
DE Alpha 1 collagen (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
.OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Ratcliffe T.A., Vitz J.R., Ray D.B.;
RT "SNP located within intron 32 of human Pro-alpha 1 (I) collagen gene
at 10,828 bp. Cysteine replaces adenine.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

Query Match Score 17%; DB 2%; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DSGGP B

Qy	7	GPEV 10	3 ; Conservative	0 ; Mismatches	1 ; Indels	0 ; Gaps	0 ;	Q96QA7	PRELIMINARY;	PRT;	10 AA.
Db	1	GPEV 4						Q96QA7	AC	DT 01-DEC-2001 (TREMBLrel. 19, Created)	
								Q96QA7	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
								Q96QA7	DT 01-JUN-2001 (TREMBLrel. 19, Last annotation update)		
								Q96QA7	DE BA51A2.1 (CC42 Guanine exchange factor (GEP) 9 (Collybistin, PEM-2, ARGEF9, HPER-2, KIAA0424)) (Fragment).		
RESULT 10								Q96QA7	GN Homo sapiens (Human).		
Q9TU33								Q96QA7	OS Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;		
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DT 01-MAY-2000	(TREMBLrel. 13, Created)							Q96QA7	RN [1].		
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DE BRCA1	(Fragment).							Q96QA7	RL EMBL; Al451106; QAC88408.1; -.		
GN Canis familiaris (Dog).								Q96QA7	FT NON_TER 10		
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RP								Q96QA7	DB 6 GGSG 9		
RX MEDLINE=20154965; PubMed=10690375;								Q9P229	RESULT 13		
RA Gray I.S., Yuzbasiyan-Gurkan V.;								Q9P229	PRELIMINARY;	PRT;	10 AA.
RT A single nucleotide (T->G) polymorphism within intron 23 of the canine BRCA1 gene.";								Q9P229	AC		
RT canine BRCA1 gene.";								Q9P229	DT 01-OCT-2000 (TREMBLrel. 15, Created)		
RL Anim. Genet. 31:76-77(2000).								Q9P229	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DR AF159258; AAD56689.1; -.								Q9P229	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
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								Q9P229	RA Biochem. Biophys. Res. Commun. 178:1413-1420(1991). EMBL; SS1343; ABAA9486.2; -.		
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								Q9P229	DR GO; GO:0005006; F:epidermal growth factor receptor activity; NAS.		
								Q9P229	DR GO; GO:0008283; P:cell proliferation; NAS.		
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DB MPRIN=METALLOENDOPEPTIDASE.								Q9QK7	OS Mus sp.		
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.								Q9QK7	RA Flannery A.V., Macadam G.C., Beynon R.J.; Biochim. Biophys. Acta 1079:119-122(1991).		
OC NCBI_TaxID=10095;								Q9QK7	RA Flannery A.V., Macadam G.C., Beynon R.J.; Biochim. Biophys. Acta 1079:119-122(1991).		
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RA Flannery A.V., Macadam G.C., Beynon R.J.; "Immunological characterisation of different meprin species in mice.";								Q9QK7	RA Flannery A.V., Macadam G.C., Beynon R.J.; Biochim. Biophys. Acta 1079:119-122(1991).		
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 DE H(-)-Translocating (Pyrophosphate-ENERGIZED) inorganic pyrophosphatase
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 OS Beta vulgaris (Sugar beet).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 OC Spermatophytina; Magnoliophytina; eudicots; core eudicots;
 OC Caryophyllales; Amaranthaceae; Beta.
 NCBI_TaxID=161934;
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 RX MEDLINE:92179265; PubMed=1311852;
 RA Sarafian V., Kim Y., Poole R.J., Rea P.A.;
 RT "Molecular cloning and sequence of cDNA encoding the pyrophosphate-
 energized vacuolar membrane proton pump of *Arabidopsis thaliana*.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).
 RL PIR; B38230; B38230.
 DR GO:0004427; F:inorganic diphosphatase activity; IEA.
 SQ SEQUENCE 10 AA; 1017 MW; 2BC8A4A87041AAA8 CRC64;
 Qy 3 GDSGG 7
 Db 3 GDTIG 7
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 AC Q9QVF0
 DT 01-MAY-2000 (TREMBrel, 13, Created)
 DT 01-MAY-2000 (TREMBrel, 13, Last sequence update)
 DT 01-JUN-2002 (TREMBrel, 21, Last annotation update)
 DE Protamine MP2 intermediate protein PMP2/5 (Fragment).
 OS Mus sp.
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 RX MEDLINE:92174934; PubMed=1541289;
 RA Chauviree M., Martineau A., Debarie M., Sautiere P., Chevallier P.;
 RT "Molecular characterization of six intermediate proteins in the
 processing of mouse protamine P2 precursor.";
 RL Eur. J. Biochem. 204:759-765(1992).
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Search completed: February 26, 2004, 09:23:29
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GenCore version 5.1.6
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 Aar0471 334 24 48.0 10 2 AAR0471
 Aar0472 335 24 48.0 10 2 AAR0472
 Aar0473 336 24 48.0 10 2 AAR0473
 Aar0474 337 24 48.0 10 2 AAR0474
 Aar0475 338 24 48.0 10 2 AAR0475
 Aar0476 339 24 48.0 10 2 AAR0476
 Aar0477 340 24 48.0 10 2 AAR0477
 Aar0478 341 24 48.0 10 2 AAR0478
 Aar0479 342 24 48.0 10 2 AAR0479
 Aar0480 343 24 48.0 10 2 AAR0480
 Aar0481 344 24 48.0 10 2 AAR0481
 Aar0482 345 24 48.0 10 2 AAR0482
 Aar0483 346 24 48.0 10 2 AAR0483
 Aar0484 347 24 48.0 10 2 AAR0484
 Aar0485 348 24 48.0 10 2 AAR0485
 Aar0486 349 24 48.0 10 2 AAR0486
 Aar0487 350 24 48.0 10 2 AAR0487
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 Aar0489 352 24 48.0 10 2 AAR0489
 Aar0490 353 24 48.0 10 2 AAR0490
 Aar0491 354 24 48.0 10 2 AAR0491
 Aar0492 355 24 48.0 10 2 AAR0492
 Aar0493 356 24 48.0 10 2 AAR0493
 Aar0494 357 24 48.0 10 2 AAR0494
 Aar0495 358 24 48.0 10 2 AAR0495
 Aar0496 359 24 48.0 10 2 AAR0496
 Aar0497 360 24 48.0 10 2 AAR0497
 Aar0498 361 24 48.0 10 2 AAR0498
 Aar0499 362 24 48.0 10 2 AAR0499
 Aar0500 363 24 48.0 10 2 AAR0500
 Aar0501 364 24 48.0 10 2 AAR0501
 Aar0502 365 24 48.0 10 2 AAR0502
 Aar0503 366 24 48.0 10 2 AAR0503
 Aar0504 367 24 48.0 10 2 AAR0504
 Aar0505 368 24 48.0 10 2 AAR0505
 Aar0506 369 24 48.0 10 2 AAR0506
 Aar0507 370 24 48.0 10 2 AAR0507
 Aar0508 371 24 48.0 10 2 AAR0508
 Aar0509 372 24 48.0 10 2 AAR0509
 Aar0510 373 24 48.0 10 2 AAR0510
 Aar0511 374 24 48.0 10 2 AAR0511
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 Aar0513 376 24 48.0 10 2 AAR0513
 Aar0514 377 24 48.0 10 2 AAR0514
 Aar0515 378 24 48.0 10 2 AAR0515
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 Aar0520 383 24 48.0 10 2 AAR0520
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 Aar0536 399 24 48.0 10 2 AAR0536
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 Aar0540 403 24 48.0 10 2 AAR0540
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 Aar0543 406 24 48.0 10 2 AAR0543
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 Aar0546 409 24 48.0 10 2 AAR0546
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 Aar0549 412 24 48.0 10 2 AAR0549
 Aar0550 413 24 48.0 10 2 AAR0550
 Aar0551 414 24 48.0 10 2 AAR0551
 Aar0552 415 24 48.0 10 2 AAR0552
 Aar0553 416 24 48.0 10 2 AAR0553
 Aar0554 417 24 48.0 10 2 AAR0554
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 Aar0556 419 24 48.0 10 2 AAR0556
 Aar0557 420 24 48.0 10 2 AAR0557
 Aar0558 421 24 48.0 10 2 AAR0558
 Aar0559 422 24 48.0 10 2 AAR0559
 Aar0560 423 24 48.0 10 2 AAR0560
 Aar0561 424 24 48.0 10 2 AAR0561
 Aar0562 425 24 4

ALIGNMENTS

RESULT 1
TEST PROCESSED. Minimum March 08

AAU78372 standard; peptide; 10 AA.
ID: AAU78372

database : AAU78372 ;
1: *-Genesee, 29900s; *-AC
XX

2: GenesectP2000s: *
 3: GenesectP2001s: *
 4: GenesectP2002s: *
 5: GenesectP2003as: *
 6: GenesectP2003bs: *
 7: GenesectP2004s: *
 8: GenesectP2004s: *
 XX Serine esterase conserved sequence #1.
 DE XX Serine esterase; osteopathic; thrombin; receptor; agonist;
 KW bone growth stimulation; osteoinduction; farm animal; companion animal;
 KW laboratory animal; bone graft; segmental bone gap; bone void;
 KW non-union fracture.

No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

סימן

result	No.	Query			DB	ID	Description
		Score	Match	Length			
1	46	92.0	10	5	AAU73372	Serine es	Aau73372 Serine es
2	46	92.0	10	5	AAU73373	Serine es	Aau73373 Serine es
3	46	92.0	10	5	AEE20156	Serine es	Aee20156 Serine es
4	46	92.0	10	5	AEE20155	Serine es	Aee20155 Serine es
5	46	92.0	10	5	ABB80261	Serine es	Abb80261 Serine es
6	46	92.0	10	7	ABB80262	Serine es	Abb80262 Serine es
7	43	86.0	10	4	AAB31464	Human mem	Aab31464 Human mem
8	32	64.0	10	4	AAG94412	Human com	Aag94412 Human com
9	29	58.0	10	2	ARR65594	Peptide f	Aar1594 Peptide f
10	29	58.0	10	2	AAR93844	N.Gonorrh	Aar16844 N.Gonorrh
11	29	58.0	10	4	AAJ01260	Hepatitis	Aaj01260 Hepatitis
12	29	58.0	10	4	AAJ07071	Hepatitis	Aaj07071 Hepatitis
13	29	58.0	10	4	AAJ01934	Hepatitis	Aaj01934 Hepatitis
14	29	58.0	10	4	AAJ01082	Hepatitis	Aaj01082 Hepatitis
15	28	56.0	10	2	AAR11746	Cyclic p1	Aar11746 Cyclic p1
16	28	56.0	10	2	AAR11747	Cyclic p1	Aar11747 Cyclic p1
17	28	56.0	10	2	AAW79650	N-alpha-A	Aaw79650 N-alpha-A
18	28	56.0	10	2	AAW79652	N-alpha-B	Aaw79652 N-alpha-B
19	28	56.0	10	2	AAW79651	N-alpha-A	Aaw79651 N-alpha-A
20	28	56.0	10	4	AAG93790	Human com	Aag93790 Human com
21	28	56.0	10	7	ADD64406	Angiopoie	Add64406 Angiopoie
22	27	54.0	10	4	AAG97589	Human com	Aag97589 Human com
23	27	54.0	10	4	AAG97790	Human com	Aag97790 Human com
24	27	54.0	10	5	AEE28776	CAS	Aee28776 CAS

AdI/888/Giuliano

RESULT 1
 AAU78372 ID AAU78372 staa
 XX AC AAU78372;
 XX DT 18-JUN-2002
 XX DE Serine ester
 XX KW Serine ester
 KW bone growth
 KW laboratory a
 KW non-union fr
 XX OS Synthetic.
 PN WO200205836
 XX PD 24-JAN-2002.
 XX PF 18-JUL-2001,
 XX PR 19-JUL-2000,
 XX PA (TEXA) UNTV
 XX PI Carney DH,
 XX DR 2002-34
 XX PT Stimulating
 PT such as a si
 PT structure, b
 XX PS Claim 6; Page
 XX CC The invention
 CC a subject to s
 CC agonist to s
 CC animal, compo
 CC osteoinducti
 CC represents a
 CC esterase the
 CC thrombin res
 XX

ALIGNMENTS

Query Match Similarity 92.0%; Score 46; DB 5; Length 10;
 Best Local Similarity 80.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX

QY 1 CXGDSGGPXY 10
 Db 1 CEGDSSGPFXV 10

RESULT 3
 AAE20156 standard; peptide; 10 AA.
 ID AAE20156;
 XX
 AC AAE20156;
 XX
 DT 18-JUN-2002 (first entry)

XX Serine esterase conserved peptide #2.
 XX Cartilage growth; cartilage repair; arthritic joint; traumatic injury;
 KW non-proteolytically activated thrombin receptor; NPAR; chondrocyte;
 KW therapy; implantation; serine esterase conserved peptide.
 XX
 Unidentified.

OS
 XX
 Key Location/Qualifiers
 FH Misc-difference 2
 PT /label= Glu, Gln
 FT Misc-difference 9
 PT /label= Phe, Met, Leu, His, Val
 XX
 WO200307748-A2.
 PN
 XX
 PD 31-JAN-2002.
 XX
 PP 19-JUL-2001; 2001WO-US022668.
 XX
 PR 20-JUL-2000; 2000US-0219800P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 Carney DH, Crowther RS, Stiernberg J, Bergmann J;
 PI
 XX
 DR WPI; 2002-268953/31.
 XX
 Stimulating growth and repair of cartilage, useful for treating e.g.,
 PR arthritis, by local administration of an agonist of non-proteolytically
 activated thrombin receptor.
 XX
 PS Claim 9; Page 25; 28pp; English.

XX
 Synthetic.
 XX
 Key Location/Qualifiers
 FH Misc-difference 2
 PT /label= Glu, Gln
 FT Misc-difference 9
 PT /label= Phe, Met, Leu, His, Val
 XX
 WO200205836-A2.
 PN
 XX
 PD 24-JAN-2002.
 XX
 PP 18-JUL-2001; 2001WO-US022641.
 XX
 PR 19-JUL-2000; 2000US-0219300P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
 XX
 WPI; 2002-303796/34.

XX
 Stimulating bone growth at a site in a subject in need of osteoinduction,
 PT such as a site of bone graft, segmental bone gap, bone void or non-union
 PT structure, by administering agonist of activated thrombin receptor.
 XX
 PS Claim 8; Page 22; 27pp; English.

XX
 The invention describes a method of stimulating bone growth at a site in
 CC a subject in need of osteoinduction. The method involves administering an
 CC agonist to stimulate bone growth at a site in a subject (e.g. a farm
 CC animal, companion animal or laboratory animal), in need of
 CC osteoinduction, such as the site in need of a bone graft in a subject, a
 CC segmental bone gap, a bone void or a non-union fracture. This sequence
 CC represents a serine esterase conserved sequence obtained from a serine
 CC thrombin receptor that can stimulate or activate the non-proteolytically activated
 XX
 Sequence 10 AA;

Query Match Similarity 92.0%; Score 46; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 CXGDSGGPXY 10
 Db 1 CXGDSGGPFXV 10

RESULT 4
 AAE20155 standard; peptide; 10 AA.
 ID AAE20155;
 XX
 AC AAE20155;
 XX
 DT 18-JUN-2002 (first entry)

XX Serine esterase conserved peptide #1.

XX Cartilage growth; cartilage repair; arthritic joint; traumatic injury;
 KW non- proteolytically activated thrombin receptor; NPAR; chondrocyte;
 KW therapy; implantation; serine esterase conserved peptide.
 XX Unidentified.

XX WO200207748-A2 .
 PN 31-JAN-2002 .
 PD XX
 PF 19-JUL-2001 ; 2001WO-US022668 .
 PR 20-JUL-2000 ; 2000US-0219800P .
 PA (TEXA) UNIV TEXAS SYSTEM .
 PI Carney DH, Crowther RS, Stiernberg J, Bergmann J;
 DR WPI; 2002-268953/31 .
 PT Stimulating growth and repair of cartilage, useful for treating e.g.,
 PT arthritis, by local administration of an agonist of non-proteolytically
 PT activated thrombin receptor .
 PS Claim 7; Page 24; 28pp; English .
 CC The invention relates to a method of stimulating growth and repair of
 CC cartilage. The method involves administering to the site, an agonist of
 CC non-proteolytically activated thrombin receptor (NPAR). The method is
 CC used in human or veterinary medicine for the treatment of arthritic
 CC joints and damage/loss of cartilage caused by traumatic injury. Also
 CC chondrocytes may be cultured in presence of NPAR agonist to provide cells
 CC for implantation at sites requiring growth/repair of cartilage. The
 CC present sequence is serine esterase conserved peptide. This sequence is
 CC present in the thrombin peptide derivatives which serve as a NPAR agonist
 XX Sequence 10 AA;

Query Match 92.0%; Score 46; DB 5; Length 10;

Best Local Similarity 80.0%; Pred. No. 18;
 Matches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGNGGGPVY 10

Db 1 CEGDSSGGPPVY 10

Sequence 10 AA;

Query Match 92.0%; Score 46; DB 5; Length 10;

Best Local Similarity 80.0%; Pred. No. 18;
 Matches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGNGGGPVY 10

Db 1 CEGDSSGGPPVY 10

Sequence 10 AA;

Query Match 92.0%; Score 46; DB 5; Length 10;

Best Local Similarity 80.0%; Pred. No. 18;
 Matches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGNGGGPVY 10

Db 1 CEGDSSGGPPVY 10

Sequence 10 AA;

Query Match 92.0%; Score 46; DB 5; Length 10;

Best Local Similarity 80.0%; Pred. No. 18;
 Matches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGNGGGPVY 10

Db 1 CEGDSSGGPPVY 10

Sequence 10 AA;

Query Match 92.0%; Score 46; DB 5; Length 10;

Best Local Similarity 80.0%; Pred. No. 18;
 Matches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGNGGGPVY 10

Db 1 CEGDSSGGPPVY 10

Sequence 10 AA;

PA (TEXA) UNIV TEXAS SYSTEM .
 XX
 PN Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
 PI Stiernberg J, Bergmann J ,
 DR WPI; 2003-721552/68 .

XX Stimulation of bone growth and cartilage formation in e.g., bone graft and
 PT arthritic joints involves administration of a thrombin derivative
 PT peptide .
 XX Disclosure; Page 8; Opp; English .
 PS

XX The sequences given in ABB80261-62 represent serine esterase conserved
 CC domains. These peptide are used as part of the thrombin peptides
 CC derivatives of the invention for stimulating bone growth. The thrombin
 CC peptides of the invention have the formula: Asp-Ala-R, where R is a
 CC serine esterase conserved domain. These peptides are used for stimulating
 CC bone growth and cartilage growth or repair in e.g., bone graft, segmental
 CC gap in a bone, bone void, at a non-union fracture, arthritic joints, and
 CC sites treated for cartilage damage or loss due to traumatic injury, and
 CC for culturing chondrocytes in vitro. The thrombin derivative peptide
 CC improves the quality of repair tissue, leads to more durable and
 CC functional restoration of joint bio mechanics, reduces the incidence of
 CC osteoarthritis in patients suffering from traumatic cartilage injuries
 CC and accelerates the rate of normal fracture healing in fracture or small
 CC gap defects .
 XX Sequence 10 AA;

Query Match 92.0%; Score 46; DB 7; Length 10;
 Best Local Similarity 80.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGNGGGPVY 10

Db 1 CEGDSSGGPPVY 10

Sequence 10 AA;

RESULT 6
 ABB80262
 ID ABB80262 standard; peptide; 10 AA.

AC ABB80262;
 AC ABB80262;

XX DT 18-DEC-2003 (first entry)

DE Serine esterase conserved sequence #2.

XX Serine esterase; conserved domain; thrombin peptide; stimulation; bone;
 KW cartilage; growth; repair; bone graft; segmental gap; bone void;
 KW non-union fracture; arthritic joint; arthritis; damage; traumatic injury;
 KW culture; chondrocyte; joint bio mechanics; osteoarthritis.
 XX Mammal sp.
 OS WO2003061690-A1 .
 OS

XX Key Difference 2
 KW Misc-difference 2
 KW Label= Glu, Gln
 KW Non-union fracture; arthritic joint; arthritis; damage; traumatic injury;
 KW culture; chondrocyte; joint bio mechanics; osteoarthritis.
 XX DT 18-DEC-2003 (first entry)
 DE Serine esterase conserved sequence #1.
 XX Serine esterase; conserved domain; thrombin peptide; stimulation; bone;
 KW cartilage; growth; repair; bone graft; segmental gap; bone void;
 KW non-union fracture; arthritic joint; arthritis; damage; traumatic injury;
 KW culture; chondrocyte; joint bio mechanics; osteoarthritis.
 XX Mammal sp.
 OS WO2003061690-A1 .
 OS

XX 31-JUL-2003 .
 XX 17-JAN-2002 ; 2002WO-US001451 .
 PA (TEXA) UNIV TEXAS SYSTEM .
 XX PR 17-JAN-2002 ; 2002WO-US001451 .
 PA Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
 PI

PI Stiernberg J, Bergmann J;
 XX WPI: 2003-721552/68.

PT Stimulation of bone growth and cartilage formation in e.g. bone graft and arthritic joints involves administration of a thrombin derivative peptide.
 XX Disclosure; Page 8; OPP; English.

CC The sequences given in ABB80261-62 represent serine esterase conserved domains. These peptide are used as part of the thrombin peptides derivatives of the invention for stimulating bone growth. The thrombin peptides of the invention have the formula: Asp-Ala-R, where R is a serine esterase conserved domain. These peptides are used for stimulating bone growth and cartilage growth or repair in e.g. bone graft, segmental gap in a bone, bone void, at a non-union fracture, arthritic joint, and sites treated for cartilage damage or loss due to traumatic injury, and for culturing chondrocytes in vitro. The thrombin derivative peptide improves the quality of repair tissue, leads to more durable and functional restoration of joint bio mechanics, reduces the incidence of osteoarthritis in patients suffering from traumatic cartilage injuries and accelerates the rate of normal fracture healing in fracture or small gap defects

XX Sequence 10 AA;

Query Match 92.0%; Score 46; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXGDSGGPVX 10
 Db 1 CXGDSGGPVX 10

RESULT 7
 AAB35464 standard; protein; 10 AA.

XX AC AAB35464;
 XX DT 06-JUN-2001 (first entry)
 XX DB Human membrane-type serine protease MT-SP1 PCR primer encoded peptide #2.
 XX KW Human; membrane-type serine protease; MT-SP1; cancer; PCR primer.
 XX OS Homo sapiens.

XX FH Key-Difference 2
 PT Misc-difference 2 /label= Ala, Ser, Thr
 PT Misc-difference 4 /label= Lys, Glu, Gln, His
 XX PN WO200123524-A2.
 XX PD 05-APR-2001.
 XX PP 02-OCT-2000; 2000WO-US027250.
 XX PR 30-SEP-1999; 99US-00410362.
 XX PA (REGC) UNIV CALIFORNIA.

XX PI Craik CS, Takeuchi T, Shuman M;
 XX DR WPI: 2001-245002/25.
 XX DR N-PSDB; AAF28096.

PT New nucleic acid encoding a membrane type serine protease, useful for the diagnosis, prognosis and treatment of cancer, particularly metastatic

PI PT cancers.
 XX PS Example 1; Page 71; 102pp; English.

CC The present invention provides the protein and coding sequences for the novel human membran-type serine protease MT-SP1. Increased expression of this protein is associated with cancer, and so the sequences can be used in cancer diagnosis and the identification of treatments. The present sequence is a peptide encoded by a PCR primer used to isolate the MT-SP1 coding sequence

XX SQ Sequence 10 AA;

Query Match 86.0%; Score 43; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXGDSGGP 8
 Db 3 CXGDSGGP 10

RESULT 8
 AAG94412 standard; peptide; 10 AA.

XX ID AAG94412
 XX AC AAG94412;
 XX DT 18-SEP-2001 (first entry)
 XX DE Human complementary peptide, SEQ ID NO: 606.
 XX KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX OS Homo sapiens.

XX PN WO200142277-A2.
 XX PD 14-JUN-2001.
 XX PR 13-DEC-2000; 2000WO-GB000776.
 XX PA 13-DEC-1999; 99GB-00029464.
 XX PA (PROT-) PROTEOM LTD.
 XX PI Roberts GW, Heal JR;
 XX DR WPI: 2001-408419/43.

CC A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.

XX PS Example 4; Page 126; 646pp; English.

XX SQ Sequence 10 AA;

Query Match 64.0%; Score 32; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 9.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXGDSGG 7
 Db 2 CXGESSGG 8

CC vaccines for the prevention and treatment of HCV infection in humans. The
 present sequence is an epitope used in the disclosure of the invention

PN WO200121189-A1.
 XX 29-MAR-2001.
 XX 19-JUL-2009; 99US-00357737.
 XX (EPIM-) EPIMMUNE INC.
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus.
 Disclosure; Page 132; 214pp; English.
 PT XX
 PS XX
 CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAU0001-AAU04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention
 CC SQ Sequence 10 AA;
 Query Match 58.0%; Score 29; DB 4; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GDSGGP B
 DB 4 GSSGGP 9
 XX RESULT 13
 AAU01934
 ID AAU01934 standard; peptide; 10 AA.
 XX
 AC AAU01934;
 XX DT 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #1925.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX OS Hepatitis C virus.
 XX PN WO200121189-A1.
 XX PD 29-MAR-2001.
 XX PF 19-JUL-2000; 2000WO-US019774.
 XX PR 19-JUL-1999; 99US-00357737.
 XX PA (EPIIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 AC Baker DM, Cellis E, Kubo RT, Grey HM;
 XX DR WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus.
 XX PS Disclosure; Page 148; 214pp; English.
 XX PR XX
 CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAU0001-AAU04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention
 XX SQ Sequence 10 AA;
 Query Match 58.0%; Score 29; DB 4; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GDSGGP B
 DB 4 GSSGGP 9
 XX RESULT 14
 AAU01082
 ID AAU01082 standard; peptide; 10 AA.
 XX
 AC AAU01082;
 XX DT 02-JUL-2001 (first entry)
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX OS Hepatitis C virus.
 XX PN WO200121189-A1.
 XX PA (EPIIM-) EPIMMUNE INC.
 XX DR WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus.
 Disclosure; Page 117; 214pp; English.
 PT XX
 PS XX
 CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAU0001-AAU04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention
 XX

DE Hepatitis C virus epitope #1073.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX Hepatitis C virus.
XX WO200121169-A1.
XX 29-MAR-2001.
XX 19-JUL-2000; 2000WO-US019774.
XX 19-JUL-1993; 99US-00357737.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis B, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX A new composition useful as a vaccines against hepatitis C virus.
XX Disclosure; Page 127; 214pp; English.
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AA0001-AA0412C
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention
CC Semenice 10
CC

```

Query Match      58 0% ; Score 29; DB 4; Length 10;
Best Local Similarity 83 3% ; Pred. NO: 2.2e+03;
Matches 5 ; Conservative 0; Mismatches 1; Indels 0; caps 0;
Y      3 GDSGGP 8
      1 GGGGGG 9

```

RESULT 15
AR11/46

X X AAR1746:
 X C
 X X 25-MAR-2003 (revised)
 X T 05-JUL-1991 (first entry)
 X X Cyclic platelet aggregation inhibitor - example #3.
 X X Myocardial infarction; deep vein thrombosis; pulmonary embolism; stroke.
 X X

X	EP425212-A.
X	02-MAY-1991.
X	22-OCT-1990 : 90EP-00
X	23-OCT-1989 : 89US-00
X	(SMIK) SMITHKLINE BEE
X	(ALIF /) ALI F E.
X	Ali FEF Samanen JM;
X	WPI; 1991-126685/18.

PT New cyclic peptide(s) with Gly-Asp sequence - useful as platelet aggregation inhibitors to treat myocardial infarction, deep vein thrombosis, pulmonary embolism, stroke etc.
 PT
 XX
 PS Claim 9; Page 44; 55PP; English.
 XX
 CC The sequence is the Peptide Part of the cpd.: N[alpha]-Ac-cyclo(S,S)-Cys-
 CC Arg-Gly-Asp-Ser-Arg-Gly-Asp-Ser-Cys-NH2 See also AARI1743; R11748 for
 CC examples. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX
 SQ Sequence 10 AA;
 Query Match 56.0%; Score 28; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.2e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;
 Qy 1 CKGDSGG 7
 Db 1 CRGBSRG 7

Result No.	Score	Query Match	Length	DB ID	Description	%
1	46	92.0	10	9	US-09-909-348-1	Sequence 1, Appli
2	46	92.0	10	9	US-09-909-348-2	Sequence 2, Appli
3	46	92.0	10	9	US-09-909-348-2	Sequence 1, Appli
4	46	92.0	10	9	US-09-909-348-2	Sequence 2, Appli
5	46	92.0	10	13	US-10-050-892-1	Sequence 1, Appli
6	46	92.0	10	13	US-10-050-892-2	Sequence 2, Appli
7	46	92.0	10	13	US-10-050-898-1	Sequence 1, Appli
8	46	92.0	10	13	US-10-050-888-2	Sequence 2, Appli
9	32	64.0	10	10	US-09-572-404B-606	Sequence 606, Appli
10	28	56.0	10	10	US-09-572-404B-584	Sequence 358A, Appli
11	27	54.0	10	10	US-09-572-404B-1784	Sequence 3784, Appli
12	27	54.0	10	10	US-09-572-404B-3785	Sequence 3785, Appli
13	26	52.0	10	9	US-09-819-957-55	Sequence 5575, Appli
14	25	50.0	10	10	US-09-572-404B-174	Sequence 174, Appli
15	25	50.0	10	10	US-09-572-404B-2027	Sequence 2027, Appli

Patent No. US2002004273A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Stierberg, Janet
 APPLICANT: Bermann, John
 TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
 FILE REFERENCE: 3033-1003-001
 CURRENT APPLICATION NUMBER: US09/909,348
 PRIOR APPLICATION NUMBER: 2001-07-19
 PRIOR FILING DATE: US 60/219,800
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of Thrombin
 NAME/KEY: VARIANT
 LOCATION: (1) ... (10)
 OTHER INFORMATION: Xaa at position two is Glu or Gln
 OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
 US-09-909-348-2

Query Match	92.0%	Score 46;	DB 9;	Length 10;
Best Local Similarity	100.0%	Pred. No. 0.28;		
Matches	10;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			0;

Db 1 CXGDSGGPXY 10
 Db 1 CXGDSGGPXY 10

RESULT 3
 US-09-909-122-1
 Sequence 1, Application US/09909122
 Patent No. US2002012802A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 FILE REFERENCE: 3033-1002-001
 CURRENT APPLICATION NUMBER: US09/909,122
 PRIOR APPLICATION NUMBER: 2001-07-19
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-122-1

Query Match	92.0%	Score 46;	DB 9;	Length 10;
Best Local Similarity	80.0%	Pred. No. 0.28;		
Matches	8;	Conservative 0;	Mismatches 2;	Indels 0;
Gaps	0;			0;

Qy 1 CXGDSGGPXY 10
 Db 1 CEGDSSGPFY 10

RESULT 4
 US-09-909-122-2
 Sequence 2, Application US/09909122
 Patent No. US2002012802A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 FILE REFERENCE: 3033-1002-001
 CURRENT APPLICATION NUMBER: US09/909,122
 PRIOR APPLICATION NUMBER: 2001-07-19
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-122-2

Query Match	92.0%	Score 46;	DB 9;	Length 10;
Best Local Similarity	80.0%	Pred. No. 0.28;		
Matches	8;	Conservative 0;	Mismatches 2;	Indels 0;
Gaps	0;			0;

Qy 1 CXGDSGGPXY 10

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RESULT 6
US-10-050-692-2
; Sequence 2, Application US/10050692
; Publication No. US20020182205A1;
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Recin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 103 1.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO: 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: human fragment of prothrombin
; FEATURE: NAME/KEY: VARIANT
; LOCATION: (2) ... (2)
; OTHER INFORMATION: Xaa = Glu or Gln
; FEATURE: NAME/KEY: VARIANT
; LOCATION: (9) ... (9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
; OTHER INFORMATION: LENGTH: 10

RESULT 7
US-10-050-688-1
; Sequence 1, Application US/10050688
; Publication No. US20020198154A1;
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Bergmann, John
; APPLICANT: Bergmann, Janet
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 303 1.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO: 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Peptide fragment of thrombin
; FEATURE: NAME/KEY: VARIANT
; LOCATION: (2) ... (2)
; OTHER INFORMATION: Xaa = Glu or Gln
; FEATURE: NAME/KEY: VARIANT
; LOCATION: (9) ... (9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
; OTHER INFORMATION: LENGTH: 10

RESULT 8
US-10-050-688-2
; Sequence 2, Application US/10050688
; Publication No. US20020198154A1;
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Bergmann, John
; APPLICANT: Bergmann, Janet
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; FILE REFERENCE: 303 1.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO: 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Peptide fragment of thrombin
; FEATURE: NAME/KEY: VARIANT
; LOCATION: (2) ... (2)
; OTHER INFORMATION: Xaa = Glu or Gln
; FEATURE: NAME/KEY: VARIANT
; LOCATION: (9) ... (9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
; OTHER INFORMATION: LENGTH: 10

RESULT 9
US-09-572-404B-606
; Sequence 606, Application US/09572404B
; Publication No. US20030078374A1;
; GENERAL INFORMATION:
; APPLICANT: Human patient
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO: 1
; LENGTH: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; TITLE OF INVENTION: Complementary Peptide Ligands from the human genome
; TITLE OF INVENTION: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Proprotein Ltd
; TITLE OF INVENTION: Complementary Peptide Ligands from the human genome
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Proprotein version 1.0

```


TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Unknown
 MOLECULE TYPE: Peptide
 FEATURE: Other
 NAME/KEY: Other
 LOCATION: 8
 OTHER INFORMATION: Undefined
 US-09-879-957-55 : SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Query Match 52.0%; Score 26; DB 9; Length 10;
 Best Local Similarity 71.4%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CXGDSGG 7
 Db 1 CMGDSIG 7

RESULT 14
 US-09-572-404B-174
 Sequence 174, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human Patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProtPatent version 1.0
 SEQ ID NO: 174
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE: Sequence located in EPHB4 OR HTK at 974-983 and may interact with
 OTHER INFORMATION: Sequence 173 in this patent.
 US-09-572-404B-174

Query Match 50.0%; Score 25; DB 10; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 GDGGP 8
 Db 5 GGTGGP 10

RESULT 15
 US-09-572-404B-2027
 Sequence 2027, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human Patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProtPatent version 1.0
 SEQ ID NO: 2027
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 09:19:44 ; Search time 15.5 Seconds
(without alignments)
33.307 Million cell updates/sec

Title: US-09-909-348-2

Perfect score: 50

Sequence: CXGDSGPXV 10

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 13857

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	26	52.0	10	4	US-08-610-915A-55	Sequence 55, Appli
2	25	50.0	10	3	US-08-933-738A-9	Sequence 9, Appli
3	25	50.0	10	3	US-08-159-339A-827	Sequence 827, Appli
4	25	50.0	10	3	US-08-713-356C-9	Sequence 9, Appli
5	25	50.0	10	4	US-09-241-268-9	Sequence 9, Appli
6	25	50.0	10	4	US-09-495-562-9	Sequence 9, Appli
7	24	48.0	10	1	PCT-US93-05428B-40	Sequence 40, Appli
8	24	48.0	10	1	US-08-340-428B-40	Sequence 16, Appli
9	24	48.0	10	3	US-08-718-323A-16	Sequence 18, Appli
10	24	48.0	10	3	US-09-010-290-6	Sequence 6, Appli
11	24	48.0	10	4	US-09-587-526-16	Sequence 16, Appli
12	24	48.0	10	4	US-09-587-526-18	Sequence 18, Appli
13	24	48.0	10	5	PCT-US93-0306-40	Sequence 40, Appli
14	23	46.0	10	5	US-08-361-864-36	Sequence 36, Appli
15	23	46.0	10	2	US-08-902-367-7	Sequence 7, Appli
16	23	46.0	10	3	US-08-535-170-9	Sequence 9, Appli
17	23	46.0	10	3	US-08-718-323A-15	Sequence 15, Appli
18	23	46.0	10	3	US-08-718-323A-17	Sequence 17, Appli
19	23	46.0	10	4	US-08-630-915A-54	Sequence 54, Appli
20	23	46.0	10	4	US-09-587-526-15	Sequence 15, Appli
21	23	46.0	10	4	US-09-587-526-17	Sequence 17, Appli
22	22	44.0	10	3	US-08-159-339A-897	Sequence 897, Appli
23	22	44.0	10	3	US-08-836-786-2	Sequence 2, Appli
24	22	44.0	10	3	US-08-480-332-9	Sequence 9, Appli
25	22	44.0	10	4	US-08-630-915A-58	Sequence 58, Appli
26	22	44.0	10	4	US-09-424-656-6	Sequence 6, Appli
27	21.5	43.0	10	3	US-08-925-002-65	Sequence 65, Appli

ALIGNMENTS

RESULT 1
US-08-630-915A-55
Sequence 55, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: POWERS, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TYPING OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penne & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-27111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 8
OTHER INFORMATION: Undefined
US-08-630-915A-55

Query Match 52.0%; Score 26; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CKEDSGG 7
 Db 1 CMEDSLG 7

RESULT 2
 US-08-293-738A-9
 Sequence 9, Application US/08993738A
 Parent No. 592B38
 GENERAL INFORMATION:
 APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;
 ATTORNEY/AGENT INFORMATION:
 Boon-Falleur, Thierry
 TITLE OF INVENTION: Isolated Peptides Which Complex With
 HLA-Cw*16 Molecules, and Uses Thereof
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski L.L.P.
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/993,738A
 FILING DATE: 19-December-1997

CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/713,354
 FILING DATE: 13-September-1996

CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 592B93Bman D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: IUD 5460.1 DIV - JEL/NDH
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 828-3884

SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 US-08-159-339A-827

Query Match 50.0%; Score 25; DB 3; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GDGGGPXV 10
 Db 2 GEGAGPPSV 9

RESULT 4
 US-08-713-3354C-9
 Sequence 9, Application US/08713354C
 Parent No. 626215

GENERAL INFORMATION:
 APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;
 ATTORNEY/AGENT INFORMATION:
 Boon-Falleur, Thierry
 TITLE OF INVENTION: Isolated Peptides Which Complex With
 HLA-Cw*16 Molecules, and Uses Thereof
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

RESULT 3
 US-08-159-339A-827
 Sequence 827, Application US/08159339A
 Parent No. 6037135

GENERAL INFORMATION:
 APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban

TITLE OF INVENTION: HLA Binding peptides and their

APPLICATION NUMBER: US/08/713,354C
 FILING DATE: 13-September-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6265215man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5460
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEX/FAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-713-354C-9

Query Match 50.0% Score 25; DB 3; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
 Db 3 SGGPRI 8

RESULT 5
 US-09-241-268-9 Application US/09241268
 Patent No. 6323028
 GENERAL INFORMATION:
 APPLICANT: van der Bruggen, Pierre; Deplaen Etienne;
 APPLICANT: Bon-Faillieur, Thierry
 TITLE OF INVENTION: Isolated Peptides Which Complex With
 TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
 NUMBER OF SEQUENCES: 12
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/495,562
 FILING DATE: 01-Feb-2000
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/241,268
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6429287man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-495,562-9

Query Match 50.0% Score 25; DB 4; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
 Db 3 SGGPRI 8

RESULT 7
 US-08-340-428B-40 Application US/083404285
 Patent No. 5648465
 GENERAL INFORMATION:
 APPLICANT: MARGOLIS, Richard U.
 APPLICANT: BAUCH, Uwe
 APPLICANT: MARGOLIS, Renee K.
 TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
 PROTEOGLYCAN
 NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brownay and Neimark
 STREET: 419 Seventh Street, N.W.
 CITY: Washington D.C.
 STATE: D.C.

Query Match 50.0% Score 25; DB 4; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

US-09-241-268-9

COUNTRY: U.S.A.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/340,428B
 FILING DATE: 14 Nov. 564856ember 1994
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/922,911
 FILING DATE: 03 August 1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Browdy, Roger L.
 REFERENCE/DOCKET NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-737-3528
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-340,428B-40

Query Match 48.0%; Score 24; DB 3; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GDSGGPXY 10
 Db 3 GDQGPRYL 1.0

RESULT 8
 US-08-718-323A-16
 Sequence 16 Application US/08718323A
 GENERAL INFORMATION:
 APPLICANT: Raymond John Owens, Martyn Kim Robinson,
 TITLE OF INVENTION: Antibodies against E-selectin,
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6204007ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/718,323A
 FILING DATE: 11 Nov. 6204007-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Trujillo, Doreen Yatko
 REGISTRATION NUMBER: 35,719
 REFERENCE/DOCKET NUMBER: CARP-0054
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 56-3439
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-718-323A-18

Query Match 48.0%; Score 24; DB 3; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXY 10
 Db 5 TGGPSV 10

RESULT 10
 US-09-010-290-6
 Sequence 6 Application US/09010290
 GENERAL INFORMATION:
 APPLICANT: Stuckle
 TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR USE IN
 TITLE OF INVENTION: THROMBUS DETECTION
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:

COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/718,323A
 FILING DATE: 11 Nov. 6204007-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Trujillo, Doreen Yatko
 REGISTRATION NUMBER: 35,719
 REFERENCE/DOCKET NUMBER: CARP-0054
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids

ADDRESSEE: Banner & Witcoff, Ltd.
 STREET: 28 State St., 28th Floor
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disquette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Wordperfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/010,290
 FILING DATE: 21-JAN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GRB914020,6
 FILING DATE: 19-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB90/00933
 FILING DATE: 18-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/659,343
 FILING DATE: 21-MAR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/963,127
 FILING DATE: 19-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/816,922
 FILING DATE: 12-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Ph.D., Kathleen A.
 REFERENCE/DOCKET NUMBER: 34,380
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-227-7111
 TELEFAX: 617-227-4399
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 US-09-010-290-6

Query Match Similarity 48.0%; Score 24; DB 3; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CXGDS 5
 Db 5 CRGDS 9

RESULT 11

US-09-587-526-16
 Sequence 16, Application US/09587526
 Patent No. 6407214
 GENERAL INFORMATION:
 APPLICANT: Raymond John Owens, Martyn Kim Robinson,
 TITLE OF INVENTION: Antibodies against E-selectin
 NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
 ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION NUMBER: US/09/587,526

FILING DATE:

US-09-587-526-16

Sequence 16, Application US/09587526
 Patent No. 6407214
 GENERAL INFORMATION:
 APPLICANT: Raymond John Owens, Martyn Kim Robinson,
 TITLE OF INVENTION: Antibodies against E-selectin
 NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
 ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

FILING DATE:

US-09-587-526-18

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/587,526
 FILING DATE:
 PRIOR APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: CARP-0054
 ATTORNEY/AGENT INFORMATION:
 NAME: Trujillo, Doreen Yatko
 REGISTRATION NUMBER: 35,719
 REFERENCE/DOCKET NUMBER: CARP-0054
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-587-526-16

Query Match Similarity 48.0%; Score 24; DB 4; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 SGGPXV 1.0
 Db 5 AGGSPSV 1.0

RESULT 12
 US-09-587-526-18
 Sequence 18, Application US/09587526
 Patent No. 6407214
 GENERAL INFORMATION:
 APPLICANT: Raymond John Owens, Martyn Kim Robinson,
 TITLE OF INVENTION: Antibodies against E-selectin
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION NUMBER: US/09/587,526

Query Match Similarity 48.0%; Score 24; DB 4; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 SGGPXV 1.0
 Db 5 AGGSPSV 1.0

RESULT 13
 US-09-587-526-18
 Sequence 18, Application US/09587526
 Patent No. 6407214
 GENERAL INFORMATION:
 APPLICANT: Raymond John Owens, Martyn Kim Robinson,
 TITLE OF INVENTION: Antibodies against E-selectin
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

Query Match 48.0%; Score 24; DB 4; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SGGPXV 10
 Db 5 TGGSV 10

RESULT 13
 PCT-US93-07306-40
 Sequence 40; Application PC/TUS9307306
 / GENERAL INFORMATION:
 / APPLICANT: MARGOLIS, Richard U.
 / APPLICANT: RAUCH, Uwe
 / APPLICANT: MARGOLIS, Renee K.
 / TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
 / NUMBER OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Browdy and Neimark
 STREET: 419 Seventh Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/07306
 FILING DATE: 03-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/922,911
 FILING DATE: 03-AUG-1992
 ATTORNEY/ AGENT INFORMATION:
 NAME: Townsend, Guy K.
 REGISTRATION NUMBER: 34, 033
 REFERENCE/DOCKET NUMBER: Margolis=1A PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-328-5197
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-07306-40

Query Match 48.0%; Score 24; DB 5; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GDGGPXPV 10
 Db 3 GDQGTTL 10

RESULT 14
 US-08-361-864-36
 Sequence 36; Application US/08361864
 / GENERAL INFORMATION:
 / APPLICANT: Dean, Richard T.
 / APPLICANT: Lister-James, John
 / TITLE OF INVENTION: Multimatic Polyvalent Antithrombotic Agents
 / NUMBER OF SEQUENCES: 37
 / CORRESPONDENCE ADDRESS:

ADDRESSEE: Allegretti & Witcoff, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: Illinois
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/361, 864
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/955, 466A
 FILING DATE: 1992/02/02
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 59704an, Kevin E
 REGISTRATION NUMBER: 35, 303
 REFERENCE/DOCKET NUMBER: 92, 668
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 910-221-3317
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..5
 OTHER INFORMATION: /label= Cyclic
 OTHER INFORMATION: /note= "The sidechain sulfur of the 1st cysteine
 OTHER INFORMATION: /note= "The sidechain sulfur atom of each cysteine
 OTHER INFORMATION: is protected by an -CH2CO- group; the C-terminal
 OTHER INFORMATION: an amide bond with the N-terminus; the Y is the D
 PEPTIDE,
 NAME/KEY: Modified-site
 LOCATION: 6..8
 OTHER INFORMATION: /label= Tc-99m-binding
 OTHER INFORMATION: /note= "The sidechain sulfur atom of each cysteine
 OTHER INFORMATION: is protected by an acetamido group; the C-terminal
 OTHER INFORMATION: cysteine is an amide"
 DS-08-361-864-36

Query Match 46.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDGG 7
 Db 3 GDCGG 7

RESULT 15
 US-08-902-367-7
 Sequence 7; Application US/08902367
 / General Information:
 / Patent No. 597845
 / General Information:
 / APPLICANT: Dean, Richard T.
 / APPLICANT: Lister-James, John
 / APPLICANT: Civitello, Edgar R.
 / Title of Invention: Imaging
 / Number of Sequences: 12
 / Correspondence Address:
 / Address: McDonnell Boehnen Hulbert & Berghoff
 / Street: 300 South Wacker Drive Seventh Floor
 / City: Chicago
 / State: Illinois

COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/902,367
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,668
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5997845nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 90,1104-W
 TELEPHONE: 312, 913, 0001
 TELEFAX: 312, 913, 0002
 TELEX:
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..3
 OTHER INFORMATION: /label= D-Tyr
 OTHER INFORMATION: /note= "The tyrosine residue is in the D-stereochemical configuration."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..5
 OTHER INFORMATION: /label= Cyclic
 OTHER INFORMATION: /note= "The sidechain sulfur of the Cys
 OTHER INFORMATION: residue is covalently linked to the amino
 OTHER INFORMATION: terminus by a -CH₂CO- group."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 8..10
 OTHER INFORMATION: /label= Tc-99m-chelator
 OTHER INFORMATION: /note= "The sidechain sulfur atoms of both Cys
 OTHER INFORMATION: residues are each protected with an
 OTHER INFORMATION: acetamidomethyl group"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: /label= Amide
 OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
 OTHER INFORMATION: amide"
 US-08-902-367-7

Query Match 46.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 80.0%; Prd: No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 GPSGG 7
 Db 3 GDCCG 7

Search completed: February 26, 2004, 09:24:50
 Job time : 16.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:31:00 ; Search time 21 Seconds
(without alignments)
18.322 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21

Sequence: 1 RGDA 4

Scoring table: BLOSUM62
GapOp 10.0 , Gapext 0.5

Searched:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 63

Minimum DB seq length: 4
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:
1: Pir1:
2: Pir2:
3: Pir3:
4: Pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	57.1	4	PT0711	T-cell receptor beta chain V-D-J region (1120-2J) - mouse (fragment)
2	11	52.4	4	S47552	T-cell receptor beta chain V-D-J region (1120-2J) - mouse (fragment)
3	8	38.1	4	D41654	C.Species: Mus musculus (house mouse)
4	8	38.1	4	PT0677	C.Species: 17-Jul-1992 #Sequence change 30-May-1997
5	7	33.3	4	FCXAA	C.Accession: PT0607; PR0674; PT0711; PT0710
6	7	33.3	4	A5844	R.Feeney, A.J.
7	7	33.3	4	A32480	J.Exp. Med. 174, 115-124, 1991
8	6	33.3	4	S09478	A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
9	6	28.6	4	A32039	A.Reference number: PT0503; PMID:92277601; PMID:1711558
10	6	28.6	4	PI0140	A.Accession: PT0607
11	6	28.6	4	140697	A.Status: translation not shown
12	6	28.6	4	A41890	A.Molecule type: mRNA
13	6	28.6	4	I30569	A.Residues: 1-4 <FE3>
14	6	28.6	4	I38888	A.Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
15	6	28.6	4	A34626	A.Accession: PR0570
16	6	28.6	4	I51049	A.Status: translation not shown
17	6	28.6	4	S39390	A.Molecule type: mRNA
18	6	28.6	4	PT0633	A.Residues: 1-4 <FE4>
19	6	28.6	4	PT0271	A.Experimental source: day 18 fetal thymus, strain BALB/c, 141-1I
20	6	28.6	4	S43959	A.Accession: PR0711
21	6	28.6	4	A53284	A.Status: translation not shown
22	6	28.6	4	PT0696	A.Molecule type: DNA
23	6	28.6	4	PT0694	A.Residues: 1-4 <FE5>
24	6	28.6	4	PT0633	A.Experimental source: newborn thymus, strain BALB/c (clones 161-2AF and 161-2AF)
25	6	28.6	4	PT0698	C.Keywords: T-cell receptor
26	6	28.6	4	PT0706	Qy 2 GD 3
27	6	28.6	4	PT0675	Db 3 GD 4
28	6	28.6	4	PT0721	RESULT 2
29	6	28.6	4	PT0566	S47552

ubiquitin - rat

C.Species: Rattus norvegicus (Norway rat)

C.Date: 07-May-1995 #Sequence change 21-Jul-1995

C.Accession: S47552

ALIGNMENTS

30	6	28.6	4	2	A26209
31	5	23.8	4	2	A02147
32	5	23.8	4	2	ECNK
33	5	23.8	4	2	S43014
34	5	23.8	4	2	I40870
35	5	23.8	4	2	A35779
36	5	23.8	4	2	FMRFamide - polych
37	5	23.8	4	2	protamine P1 - ora
38	5	23.8	4	2	protamine P1 - Cer
39	5	23.8	4	2	protamine P1 - sav
40	4	19.0	4	2	thyroglobulin - do
41	4	19.0	4	2	carbon-monoxide de
42	4	19.0	4	2	gamma subunit of P
43	4	19.0	4	2	glucan 1,4-alpha-g
44	4	19.0	4	2	neuropeptide Antho
45	4	19.0	4	2	T-cell receptor be

R; Hubbard, M.J.; Carne, A.
Biophys. Acta 1200, 191-196, 1994
A; Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
A; Reference number: S47552; MUID:8031840
A; Accession: S47552
A; Molecule type: protein
A; Residues: 1-4 <RUE>
Query Match 52.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RG 2
Db 2 RG 3

RESULT 3
D41654 hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
C;Species: Haemophilus parainfluenzae.
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
C;Accession: D41654
R;Kroll, J.S.; Langford, P.R.; Lyons, B.M.
J; Bacteriol. 173, 7449-7457, 1991
A; Title: Copper/zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para
A; Reference number: A41654; MUID:92041655; PMID:1938942
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-4 <KR>>

Query Match 38.1%; Score 8; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RGD 3
Db 2 RFD 4

RESULT 4
PT0677 T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0677
R;Peeney, A.J.
J. EXP. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0558
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-4 <FE>>
A; Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG
A; Accession: PT0677
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-4 <FE2>>
A; Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH
C;Keywords: T-cell receptor
Query Match 38.1%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GD 3
Db 3 GB 4

RESULT 5
EC2AA antho-RFamide neuropeptide - sea anemone (*Anthopleura elegantissima*)
C;Species: *Anthopleura elegantissima*
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
C;Accession: A26666
R;Grimmellhuizen, C.J.P.; Graaff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A;Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anemone
A; Reference number: A26666; MUID:87092339; PMID:2879288
A; Accession: A26666
A; Molecule type: protein
A; Residues: 1-4 <GR>>
C;Comment: The function of this peptide is not known but it could act as a transmitter or a modulator of natural peptides with identical properties.
C;Superfamily: RFamide neuropeptide
C;Keywords: amidated carboxyl end, neuropeptide; pyroglutamic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl carboxylic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental
Query Match 33.3%; Score 7; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RG 2
Db 1 QG 2

RESULT 6
A23844 auto-RP amide neuropeptide - sea pansy (*Renilla koellikeri*)
C;Species: *Renilla koellikeri* (Koeilker's sea pansy)
C;Date: 21-May-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
C;Accession: A25844
R;Grimmellhuizen, C.J.P.; Groeger, A.
FEBS Lett. 211, 105-108, 1987
A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renilla
A; Reference number: A25844
A; Molecule type: protein
A; Residues: 1-4 <GR1>>
C;Keywords: amidated carboxyl end, neuropeptide; pyroglutamic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl carboxylic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental
Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RG 2
Db 1 QG 2

RESULT 7
A32480 achatin-I - Giant African snail
N; Contains: achatin-II
C;Species: *Achatina fulica* (giant African snail)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
C;Accession: A32480
R;Komatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from *Achatina fulica* fera
A; Reference number: A32480; MUID:89273551; PMID:2557281
A; Accession: A32480
A; Molecule type: protein
A; Residues: 1-4 <RAM>
A; Note: stereochemistry of the active form confirmed by chemical synthesis
P;Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto F.; Ishida, T.; In, Y.;
FEBS Lett. 307, 253-256, 1992
A;Title: Effect of the D-2ne(2) residue on molecular conformation of an endogenous neuro

(H-Gly-Phe-Ala-Asp-OH) A44691; MUID:92354723; PMID:1644179
 A; References: amination: X-ray crystallography, 0.85 angstroms
 A; Note: achatin-II has L-phenylalanine
 C; Keywords: D-amino acid
 F; Modified Site: D-phenylalanine (Phe) #status experimental

Query Match	33.3%;	Score 7;	DB 2;	Length 4;
Best Local Similarity	66.7%;	Pred. No.	2.8e+05;	
Matches	2;	Conservative	0;	Mismatches 1;
Qy	2 GDA 4			Indels 0;
Db	1 GFA 3			Gaps 0;

RESULT 8
 S09478
 Globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
 N; Alternative names: 11S globulin alpha subunit gamma chain
 C; Species: Cucurbita sp. (cucurbit)
 C; Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
 C; Accession: S09478
 R; Ohmiya, M.; Hara, I.; Matsubara, H.
 Plant Cell Physiol. 21, 157-167, 1980
 A; Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
 A; Reference number: S09056
 A; Accession: S09478
 A; Molecule type: protein
 A; Residues: 1-4 <CHN>

Query Match	33.3%;	Score 7;	DB 2;	Length 4;
Best Local Similarity	50.0%;	Pred. No.	2.8e+05;	
Matches	1;	Conservative	1;	Mismatches 0;
Qy	1 RG 2			Indels 0;
Db	2 QG 3			Gaps 0;

RESULT 9
 A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C; Species: Bos primigenius taurus (cattle)
 C; Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
 C; Accession: A32039
 R; Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989
 A; Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
 A; Accession: A32039; MUID:89123285; PMID:2563371
 A; Molecule type: protein
 A; Residues: 1-4 <HOR>
 A; Experimental source: brain
 C; Superfamily: unassigned animal peptides
 C; Keywords: amidated carboxyl end (Gly) #status experimental
 F; 4/Modified site: amidated carboxyl end

Query Match	28.6%;	Score 6;	DB 2;	Length 4;
Best Local Similarity	100.0%;	Pred. No.	2.8e+05;	
Matches	1;	Conservative	0;	Mismatches 0;
Qy	2 G 2			Indels 0;
Db	4 G 4			Gaps 0;

RESULT 10
 PL0140
 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydehydrogenase
 C; Species: Pseudomonas carboxydehydrogenase
 C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
 C; Accession: PL0140

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
 C;Accession: T30569
 R;Morrise, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
 Curr. Genet., 34, 379-385, 1998
 A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergillus
 A;Reference Number: Z30869; MUID:99087906; PMID:9871120
 A;Accession: T30569
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-4 <MOR>
 A;Cross-references: EMBL:Y15996; NID:e1285512; PID:e1216041; PIDN:CAA75927.1

Query Match 28.6%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 G 2
 Db 2 G 2

RESULT 14

I38888
 COI intron 16 protein - Podospora anserina mitochondrion
 C;Species: mitochondrion Podospora anserina
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
 C;Accession: I38888
 R;Cummings, D.J.; Michel, F.; McNally, K.L.
 Curr. Genet., 381-406, 1989
 A;Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mi
 A;Reference number: A48327; MUID:90124722; PMID:2558809
 A;Accession: I38888
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-4 <CUM>
 A;Cross-references: GB:X55026; GB:M30937; GB:M61734
 C;Genetics:
 A;Genome: mitochondrion
 A;Genetic code: SG3
 C;Keywords: mitochondrion

Query Match 28.6%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 G 2
 Db 3 G 3

RESULT 15

A34626
 RPCH-related neuropeptide - ferruginous spindle
 C;Species: Fusinus ferrugineus (ferruginous spindle)
 C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
 C;Accession: A34626
 R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
 Biochem. Biophys. Res. Commun. 167, 273-279, 1990
 A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
 A;Reference number: A34626; MUID:90179762; PMID:2310394
 A;Accession: A34626
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-4 <KUR>
 C;Keywords: neuropeptide

Query Match 28.6%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 G 2
 Db 3 G 3

Search completed: February 26, 2004, 09:34:52
 Job time : 22 secs

GenCore version 5.1.6
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OM Protein - Protein search, using sw model

Run on: February 26, 2004, 09:24:55 : Search time 12 Seconds
 (without alignments)
 17.357 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21 RGDA 4

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 5207155 residues

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 4
 Maximum DB seq length: 4

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42.4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	12	P5B618	57.1	4	OCTMI octopus min
2	7	P23594	33.3	4	ACH1 achatina fu
3	6	P19916	28.6	4	Pseudomonas
4	6	P02711	28.6	4	homo sapien
5	6	P58619	28.6	4	octopus min
6	5	P42562	23.8	4	hirudo medi
7	5	P42563	23.8	4	P42561 hirudo medi
8	5	P58707	23.8	4	anthopleura
9	5	P01162	23.8	4	macrocallis
10	5	P58706	23.8	4	anthopleura
11	5	P01858	23.8	4	homo sapien
12	4	P19918	19.0	4	pseudomonas
13	4	P58705	19.0	4	anthopleura
14	4	P36515	19.0	4	sachcharomyces
15	1	P0M01	4.8	1	YEAST

ALIGNMENTS

RESULT 1	OCPI1_OCTMI	ID	OCPI1_OCTMI	STANDARD;	PRT;	4 AA.
	AC	P58648;				
	DT	28-FEB-2003	(Rel. 41, Created)			
	DT	28-FEB-2003	(Rel. 41, Last sequence update)			
	DT	15-MAR-2004	(Rel. 43, Last annotation update)			
	DE	Cardioactive peptides Ocp-1/Ocp-2.				
	OS	Octopus minor (Octopus).				
	OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea;				
	OC	Opisthokonts; Ciliophora; Inciliata; Octopoda; Incirrata; Octopodidae;				
	OX	NCBI_TaxID=89766;				
	RN	[1]				

SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 TISSUE=Brain;
 MEDLINE=2036815; PubMed=10856044;
 Iwakuchi B.; Hisada M.; Minakata H.;
 "Cardioactive peptides isolated from the brain of a Japanese octopus,
 Octopus minor.", Peptides 21:623-630(2000).
 "Cardioactive; has both positive chronotropic and
 inotropic effects on the heart. Ocp-2 is a 1000 time less
 active than Ocp-1."
 SUBCELLULAR LOCATION: Secreted.
 PMW: Ocp-2 has L-Phe instead of D-Phe.
 MASS SPECTROMETRY: Mn=395.2; METHOD=MALDI.
 Hormone; D-amino acid.
 MOD RES 2 D-PHENYLALANINE (IN OCP-1).
 SEQUENCE 6AA879C810000000 CRC64;

Query Match 57.1%; Score 12; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.4e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3
 Db 3 GD 4

RESULT 2
 ID ACH1_ACHFU STANDARD; PRT; 4 AA.
 AC P55941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE Achatin-I
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Sigmucochira; Achatinoidea; Achatinidae; Achatina.
 NCBI_TaxID=65302;
 OX [1]

SPIONE, CHARACTERIZATION, AND SYNTHESIS.
 RP STRAIN=Ferussac; TISSUE=Ganglion;
 RC STRAIN=Ferussac; TISSUE=Ganglion;
 RX PMID=8923555; PubMed=159781;
 RA Kamatani Y.; Minakata H.; Kenny P.T.M.; Iwashita T.; Watanabe K.,
 Funase K.; Sun X.P.; Yongkiri A.; Kim K.H.; Novales-Li P.,
 RA Novales A.; Kanapi C.G.; Takeuchi H.; Nomoto K.;
 RA "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatin
 fulica Ferussac containing a D-amino acid residue";
 RT Achatin fulica, and its possible function";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 [2]

CHARACTERIZATION
 RP STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Iwashita T.; Nomoto K.; Ishida T.; In Y.; Doi M.; Inoue M.,
 RA "Crystal structure and molecular conformation of achatin-I
 (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 D-amino acid residue.",
 RT Int. J. Pept. Protein Res. 39:258-264 (1992).
 RL "Function: Neuroexcitatory peptide; increases the impulse frequency
 and produces peptide broadening of the identified heart excitatory
 neuron (PON); also enhances the amplitude and frequency of the
 heart beat. Has also an effect on several other muscles."
 CC DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 MOD RES 2 D-PHENYLALANINE.
 FT [FT]

RESULT 3
 DCML_PSECH STANDARD PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
 DE CUTL.
 OS Pseudomonas carboxydehydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OC NCBI_TaxID:290;
 RN [1]
 RP SEQUENCE;
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herrwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in carboxydrotrophic bacteria.";
 RT Arch. Microbiol. 152:335-341 (1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor; PLO140; PLO140.
 CC -!- COFACTOR: Molybdenum (molybdopterin).
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.
 DR PIR; PLO140; PLO140.
 RW Oxidoreductase; Molybdenum.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E87F000000 CRC64;
 Query Match Similarity 33.3%; Score 6; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Eosinophilactic peptides.
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE;
 RX MEDLINE=76078412; PubMed=1060033;
 RA Goetzl E.J., Austen K.F.;
 RT "Purification and synthesis of eosinophilactic tetrapeptides of human lung tissue: identification as eosinophil chemoattractant factor of anaphylaxis.";
 RT Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127 (1975).
 RESULT 4
 EOSI_HUMAN STANDARD PRT; 4 AA.
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Eosinophilactic peptides.
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE;
 RX MEDLINE=76078412; PubMed=1060033;
 RA Goetzl E.J., Austen K.F.;
 RT "Purification and synthesis of eosinophilactic tetrapeptides of human lung tissue: identification as eosinophil chemoattractant factor of anaphylaxis.";
 RT Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127 (1975).
 RESULT 5
 OCP3_OCTMI STANDARD PRT; 4 AA.
 AC P586749;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cardiotoxic Peptides Ocp-3/Ocp-4.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Coleoidea; Neocoelioidea; Octopoda; Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OC NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RX TISSUE_Brain;
 RA Iwakoshi B., Hisada M., Minakata H.;
 RT "Cardiotoxic peptides isolated from the brain of a Japanese octopus, Octopus minor.";
 RL Peptides 21:623-630 (2000).
 RL "Cardiotoxic peptides isolated from the brain of a Japanese octopus, Octopus minor.";
 CC -!- FUNCTION: Cardiotoxic; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active than Ocp-3.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -!- MASS SPECTROMETRY: MN=395.2; METHOD-MALDI.
 KW Hormone; D-amino acid.
 MOD RES 2 2
 SQ SEQUENCE 4 AA; 463 MW; 6AB365BB10000000 CRC64;
 Query Match Similarity 28.6%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 PAR3_HIRME STANDARD PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMFamamide-like neuropeptide Y/FRF-amide.
 OS Hirudo medicinalis (Medicinal leech)
 OC Eukaryota; Metazoa; Annelida; Cliteiliata; Hirudinida; Hirudinea;
 OC Arthropodabdelida; Hirudiniformes; Hirudinidae; Hirudo.
 OC NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE;

RESULT 7
ID_FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DB Peptides: "Identification of RPamide neuropeptides in the medicinal leech."
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudo.
OC Arthropoda; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RPamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908 (1991).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
Family.
KW Neuropeptide; Amidation.
FT MOD RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 598 MW; 69D073B3000000 CRC64;
Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 R 1
Db 3 R 3

RESULT 7
ID_FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DB Peptides: "Identification of RPamide neuropeptides in the medicinal leech."
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudo; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RPamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908 (1991).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
Family.
KW Neuropeptide; Amidation.
FT MOD RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 616 MW; 69D068B3000000 CRC64;
Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 R 1
Db 3 R 3

RESULT 8
FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRFamide
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudo.
OC Arthropoda; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE:H.medicinalis;
RC SPECIES=H.medicinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RPamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908 (1991).
[2]

RESULT 9
FLRN_ANTEL STANDARD; PRT; 4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Antho-Rhamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria.
OC Nyanthinae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=197354;
RA Grimminkhuizen C.J.P., Rinehart K.L. Jr., Jacob B., Graff D., Reinschmid R.K., Notthacker H.-P., Staley A.L., RT "Isolation of L-phenylalactyl-t-leu-Arg-Asn-NH₂ (Antho-RNamide), a sea anemone neuropeptide containing an unusual amino-terminal blocking group." Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
RL CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD RES 1 1
FT MOD-RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 R 1
Db 3 R 3

RESULT 10
FLRF_MACNI STANDARD; PRT; 4 AA.
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocallista nimboosa (Sun-ray clam), Nereis virens (Sandworm), Hirudo medicinalis (Medicinal leech), and OS Helisoma trivolvis (Snail).
OS Helisoma trivolvis (Snail).

Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Veneridae; Venerinae; Macrocallista.
[1] - NCBI_TaxID=5594; 6353; 6421; 2715;

SEQUENCE, AND SYNTHESIS.
SPECIES=M.nimbosa; TISSUE=Cerebral Pedal, and Visceral ganglion;
MEDLINE=72215956; PubMed=877582;

Price D.A.; Greenberg M.J.;
"Structure of a moluscan cardioexcitatory neuropeptide.";
Science 197:670-671 (1977).

RN [2]

SEQUENCE, AND CHARACTERIZATION.
SPECIES=M.nimbosa; TISSUE=Ganglion;
MEDLINE=78012038; PubMed=909875;

Price D.A.; Greenberg M.J. ;
"Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc.";
J. Biol. Chem. 7:261-281(1977).

RN [3]

SEQUENCE.
SPECIES=N. virens;
MEDLINE=90255866; PubMed=2342992;

Krajniak K.G.; Price D.A. ;
"Authentic FMRFamide is present in the polychaete *Nereis virens*.";
Peptides 11:75-77(1990).

RN [4]

SEQUENCE.
SPECIES=H. medicinalis;
MEDLINE=92193954; PubMed=1686932;

RA Evans B.D.; Pohl J.; Kartsonis N.A.; Calabrese R.L. ;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908 (1991).

RN [5]

SEQUENCE.
SPECIES=H. trivittata; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;

RA Madrid K.P.; Price D.A.; Greenberg M.J.; Khan H.R.; Saleuddin A.S.M. ;
RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma trivittata*";
Peptides 15:31-36(1994).

RN [6]

CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of cardiac contraction.

CC -!- SIMILARITY: Belongs to the PARP (FMRFamide related peptide) family.

DR PIR: A01426; ECNK.
DR PIR: A60418; A60418.
XW Neuropeptide; Amidation.

PT MOD RES 4 AA; 4 AMIDATION.

SQ SEQUENCE 4 AA; 600 MW; 6940699A000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 3 R 3

SEQUENCE.
SPECIES=H. trivittata; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;

RA Madrid K.P.; Price D.A.; Greenberg M.J.; Khan H.R.; Saleuddin A.S.M. ;
RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma trivittata*";
Peptides 15:31-36(1994).

RN [7]

CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of cardiac contraction.

CC -!- SIMILARITY: Belongs to the PARP (FMRFamide related peptide)

CC Family.

DR PIR: A01426; ECNK.
DR PIR: A60418; A60418.
XW Neuropeptide; Amidation.

PT MOD RES 4 AA; 4 AMIDATION.

SQ SEQUENCE 4 AA; 600 MW; 6940699A000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 3 R 3

SEQUENCE.
SPECIES=M.nimbosa; TISSUE=Ganglion;
MEDLINE=92270459; PubMed=1621096;

RA Nothacker H.-P.; Rinnehart K.L. Jr.; McFarlane I.D.;
Grimmeliukhuijen C.J.P. ;
"Isolation of two novel neuropeptides from sea anemones: the unusual biologically active L-3-phenylalactyl-Tyr-Arg-Lys-NH₂ and its des-phenylalactyl fragment Tyr-Arg-Lys-NH₂.";
RJ Peptides 12:1165-1173(1991).

RN [8]

FUNCTION.
MEDLINE=23391436; PubMed=8397415;

RA McFarlane I.D.; Hudman D.; Nothacker H.-P.; Grimmeliukhuijen C.J.P. ;
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-kaamide and Antho-Riamide.";
RJ Proc. R. Soc. Lond. B. Biol. Sci. 253: 183-188(1993).

RJ -!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Neuron specific.

CC Neuropeptide; Amidation.

RN KW

PT CHAIN 1 4 ANTHO-RIAMIDE I.
PT CHAIN 2 4 ANTHO-RIAMIDE II.
PT MOD RES 1 1 L-3-PHENYLALACTYL.
PT MOD RES 4 4 AMIDATION.

SQ SEQUENCE 4 AA; 598 MW; 60441B59A000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 3 R 3

RESULT 12
TUFT_HUMAN STANDARD; PRT; 4 AA.

ID TUFT_HUMAN STANDARD; PRT; 4 AA.

AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DB Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;

RP IMMUNOGLOBULIN CLASS.
RA Ridalgo B.V.; Naijjar V.A.; PubMed=4169272;

RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;

RA Nishioka K.; Constandopoulou A.; Satoh P.S.; Naijjar V.A.; "The physiological role of the lymphoid system VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";

CC Biochemistry 6:3386-3392(1996).
-!- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils in the blood. Leucokinase on the membrane releases the active peptide tuftsin from the gamma chain. Tuftsin is essential for maximum stimulation of the phagocytic activity of neutrophils.

CC DR PIR: A02147; A02147.

DR MIM: 191150; -
GO: GO:0006909; P:phagocytosis; NAS.

DR GO: GO:003823; P:antigen binding; NAS.

SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

RN [1]

Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 R 1
 Db 4 R 4

RESULT 13
 DCMS_PSECH STANDARD PRT; 4 AA.

ID DCMS_PSECH
 AC P19978;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last Sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxyhydrogena.
 OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OC NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck T., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in carboxydrophic bacteria.";
 RL Arch Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: catalyzes the oxidation of carbon monoxide to carbon dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.
 CC -!- COFACTOR: Binds 2 Fe-2S clusters.
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.
 DR PIR; PL0146; PL0146;
 KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 420 MW; 6DD3DD6P000000 CRC64;

Query Match 19.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 A 4
 Db 2 A 2

RESULT 14
 PPEKA_ANTEL STANDARD PRT; 4 AA.

ID PPEKA_ANTEL
 AC P58705;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-Kramide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nyanthaeae; Actiniidae; Anthopleura.
 OC NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=2028852; PubMed=1681803;
 RA Nothacker H.-P., Rinchart K.L. Jr., Grimmelkuijzen C.J.P.;
 RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kramide), a novel neuropeptide from sea anemones";
 RT Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 RN [2]
 RP FUNCTION

RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelkuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Kramide and Antho-RKamide.";
 RL Proc. R. Soc. Lond. B, Biol. Sci. 253:183-188 (1993).
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron specific.
 DR PIR; JQ1273; JQ1273.
 KW Neuropeptide; Amidation.
 MOD RES 1 1
 PT AMIDATION.
 SQ SEQUENCE 4 AA; 512 MW; 6DD239C940000000 CRC64;

Query Match 19.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 A 4
 Db 4 A 4

RESULT 15
 RM01 YEAST STANDARD PRT; 4 AA.

ID RM01 YEAST
 AC P3615;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (rmlL1) (Fragment).
 GN MRPL1.
 OS Saccharomyces cerevisiae (Baker's yeast)
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomyces.
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4332;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=31285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Krift V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.";
 RL FEBS Lett. 284:51-56(1991).
 DR PIR; S17255; S17255.
 DR SGD; L0002681; MRPL1.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5DD0000000 CRC64;

Query Match 4.8%; Score 1; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 A 4
 Db 1 S 1

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Page 2

Job time : 39 secs

QY	1	RGDA 4	DE Thrombo-spondin 1 RGD cell binding region.
Db	1		XX Tat region; nucleic acid-binding group; cell transfection system;
			KW gene therapy; cancer; thrombo-spondin 1.
			XX Unidentified.
RESULT 2			OS
AAB86859	standard;	peptide; 4 AA.	XX
ID			PN US6376248-B1.
XX			XX
AAB86859;			PD 23-APR-2002.
XX			XX
DT 28-NOV-2001	(first entry)		PF 16-MAR-1998; 918US-00039780.
XX			XX
DE Transport molecule/ligand binding-associated peptide #5.			PR 14-MAR-1997; 917US-00818200.
XX			XX
KW Transport molecule; ligand; cancer treatment; autoimmune disease; inflammation; infection.			PA (LIFE-) LIFE TECHNOLOGIES INC.
XX			XX
Hawley-Nelson P, Lan J, Shih P, Jesseee JA, Schifferli KP; Gebeyehu G, Ciccarone VC, Evans KL;			PI
OS Synthetic.			XX
XX			DR 2002-680647/73.
PN WO200168142-A1.			XX
XX			XX New peptide comprising Tat sequence linked to nucleic acid-binding group, e.g. in gene therapy, for improving cell-transfection efficiency.
PD 20-SEP-2001.			XX
XX			XX Example 1; Col 65; 108bp; English.
PP 13-MAR-2001; 2001WO-EP002833.			PS
XX			XX The invention relates to a peptide comprising Tat sequence linked to nucleic acid-binding group. Peptides of the invention are used as components of a cell transfection system particularly for gene therapy (especially of cancer). The present sequence is thrombo-spondin 1 RGD cell binding region. This peptide is used in the exemplification of the invention.
PR 13-MAR-2000; 2000DE-01012120.			XX
XX			XX
(KBTB-) KTB TUMORFORSCHUNGS GMBH.			XX
PA Kratz F;			XX
PT			XX
DR WPI; 2001-589998/66.			XX
XX			XX New ligand, comprising therapeutic or diagnostic agent bonded non-covalently with substance having high affinity to transport molecule.
PS Disclosure; Page 39; 74pp; German.			XX
XX			XX
CC This invention describes novel ligands which bind to transport molecules, comprising a therapeutic and/or diagnostic agent (A) non-covalently bonded via a linkage cleavable in vivo depending on pH and/or enzymatically with a substance (B) having an association constant KA to a transport molecule of above $10^{3} M^{-1}$, is new. The medicaments are especially useful for the treatment of cancers, autoimmune diseases, acute and chronic inflammation and infections caused by viruses or microorganisms. The diagnostic kits are useful for the detection of these illnesses and for the detection of the transport molecule and/or its distribution in vivo. The ligands have excellent solubility in the medium at the site of action and are easy and inexpensive to cover into adducts, as the interaction with the transport material is physical.	XX		
CC AAB8843-AAB86920 represent peptides used to illustrate the method of the invention.			XX
CC			DE Thrombin peptide derivative #1.
XX			XX
SQ Sequence 4 AA;			XX
XX			XX Thrombin; osteopathic; receptor; agonist; bone growth stimulation; osteoinduction; farm animal; companion animal; laboratory animal; bone graft; segmental bone gap; bone void; non-union fracture.
Query Match Score 21; DB 4; Length 4;			XX
Best Local Similarity 100.0%; Pred. No. 1.4e+06;			XX
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			XX
QY 1 RGDA 4			XX Synthetic.
Db 1 RGDA 4			XX
RESULT 3			XX
AAE28393	standard;	peptide; 4 AA.	PN WO2005836-A2.
ID AAE28393			XX
XX			PD 24-JAN-2002.
AC AAE28393;			XX
XX			PR 18-JUL-2001; 2001WO-US022641.
DT 27-DEC-2002	(first entry)		XX
XX			XX 19-JUL-2000; 2000US-0219300P.
			PA (TEXA) UNIV TEXAS SYSTEM.
			PI Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
			XX

DR; WPI; 2002-303796/34.
 XX Stimulating bone growth at a site in a subject in need of osteoinduction, such as a site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated thrombin receptor.

PT; Page 9; Page 22; 27pp; English.

XX The invention describes a method of stimulating bone growth at a site in a subject in need of osteoinduction. The method involves administering an agonist to stimulate bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoinduction, such as the site in need of a bone graft in a subject, a segmental bone gap, a bone void or a non-union fracture. This sequence represents a thrombin peptide derivative obtained from a serine esterase that can stimulate or activate the non-proteolytically activated thrombin receptor.

XX Sequence 4 AA;

Query Match	100.0%	Score 21;	DB 5;	Length 4;
Best Local Similarity	100.0%	Pred. No.	1.4e+06;	
Matches	4;	Conservative	0;	Mismatches 0;
AC	AAE20157;	Indels	0;	Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 5
 AAM50856 standard; Peptide; 4 AA.
 ID AAM50856
 AC
 XX DT 01-MAY-2002 (first entry)
 DE Thrombin receptor binding domain used for cardiac tissue repair.
 KW Thrombin receptor binding domain; thrombin; revascularisation;
 KW vascular occlusion; tissue repair; vulnerable; vasotropic; cardiotrop;
 KW angiogenesis; restenosis; therapy; human.
 XX Homo sapiens.
 OS WO200204008-A2.
 PN DR 17-JAN-2002.
 PD 12-JUL-2001; 2001WO-US021944.
 PR 12-JUL-2000; 2000US-0217583P.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA Carney DH; Crowther RS; Stieremberg J; Bergmann J;
 PI XX
 DR WPI; 2002-268953/31.
 XX Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteolytically activated thrombin receptor.

XX Claim 10; Page 25; 28pp; English.

XX The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (NPAR). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide. The derivatives of thrombin peptide which serves as a NPAR agonist

XX Sequence 4 AA;

Query Match	100.0%	Score 21;	DB 5;	Length 4;
Best Local Similarity	100.0%	Pred. No.	1.4e+06;	
Matches	4;	Conservative	0;	Mismatches 0;
AC	AAE20157	Indels	0;	Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDA 4

CC formulated as a sustained release formulation. It is used in claimed methods of stimulating revascularisation, stimulating vascular endothelial cell proliferation, inhibiting vascular occlusion, and inhibiting restenosis following balloon angioplasty, in which case the peptide may be coated onto the catheter

XX SQ Sequence 4 AA;

Query Match	100.0%	Score 21;	DB 5;	Length 4;
Best Local Similarity	100.0%	Pred. No.	1.4e+06;	
Matches	4;	Conservative	0;	Mismatches 0;
AC	AAE20157 standard; peptide; 4 AA.	Indels	0;	Gaps 0;

XX DT 18-JUN-2002 (first entry)
 DE Human thrombin Peptide.

XX Cartilage growth; cartilage repair; arthritic joint; traumatic injury; non-proteolytically activated thrombin receptor; NPAR; chondrocyte; therapy; implantation; thrombin Peptide; human.

XX XX
 XX Homo sapiens.

XX OS WO200207748-A2.
 PN XX
 PD 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US022668.
 PR 20-JUL-2000; 2000US-021980P.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Carney DH; Crowther RS; Stieremberg J; Bergmann J;
 XX DR WPI; 2002-268953/31.
 XX Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteolytically activated thrombin receptor.

XX Claim 10; Page 25; 28pp; English.

XX The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (NPAR). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide. The derivatives of thrombin peptide which serves as a NPAR agonist

XX SQ Sequence 4 AA;

Query Match	100.0%	Score 21;	DB 5;	Length 4;
Best Local Similarity	100.0%	Pred. No.	1.4e+06;	
Matches	4;	Conservative	0;	Mismatches 0;
AC	AAE20157	Indels	0;	Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 7
 ADA44893 standard; peptide; 4 AA.
 ID ADA44893;
 XX
 AC ADA44893;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human thrombin receptor binding domain SEQ ID NO: 1.
 XX
 human; cardiac tissue repair; angiogenic thrombin derivative peptide;
 XX
 vaso tropic; cardiac; cardiac tissue repair; revascularisation;
 XX
 vascular endothelial cell proliferation; restenosis; balloon angioplasty;
 XX
 vascular occlusion; stent coating; myocardium repair;
 XX
 angiogenic proliferation; angiogenic migration; ischaemic heart tissue;
 XX
 thrombin binding receptor.
 XX
 Homo sapiens.
 XX
 WO2003061689-A1.
 XX
 PD 31-JUL-2003.
 XX
 PP 16-JAN-2002; 2002WO-US001396.
 XX
 PR 16-JAN-2002; 2002WO-US001396.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Carney DH;
 XX
 PN WO2003061689-A1.
 XX
 PD 31-JUL-2003.
 XX
 PR 16-JAN-2002; 2002WO-US001396.
 XX
 PS Disclosure; Page 9; OPP; English.
 XX
 CC The sequences given in ABB80263-65 represent thrombin derivative peptides
 CC of the invention. The thrombin derivative peptides of the invention have
 CC the formula: Asp-Ala-R, where R is a serine esterase conserved domain.
 CC These Peptides are used for stimulating bone growth and cartilage growth
 CC or repair in e.g. bone graft, segmental gap in a bone, bone void, at a
 CC non-union fracture, arthritic joints, and sites treated for cartilage
 CC damage or loss due to traumatic injury, and for culturing chondrocytes in
 CC vitro. The thrombin derivative peptide improves the quality of repair
 CC tissue, leads to more durable and functional restoration of joint bio
 CC mechanics, reduces the incidence of osteoarthritis in patients suffering
 CC from traumatic cartilage injuries and accelerates the rate of normal
 CC fracture healing in fracture or small gap defects
 XX
 SQ Sequence 4 AA;
 CC
 DR 2003-663365/62.
 XX
 PT Use of a physiologically functional equivalent of an angiogenic thrombin
 derivative peptide for e.g. promoting cardiac tissue repair or inhibiting
 PT restenosis in a patient following balloon angioplasty.
 XX
 PS Claim 2; Page 20; 14pp; English.
 XX
 CC The invention relates to a novel method for promoting cardiac tissue
 CC repair, involving administration of a physiologically functional
 CC equivalent of an angiogenic thrombin derivative peptide. The method of
 CC the invention has vasotropic and cardiac activity. The peptides are
 CC useful for promoting cardiac tissue repair, for stimulating
 CC revascularisation or vascular endothelial cell proliferation, inhibiting
 CC restenosis in a patient following balloon angioplasty, inhibiting
 CC vascular occlusion, and for coating a stent. The peptides are also useful
 CC for promoting myocardium repair. The thrombin derivative peptides induce
 CC angiogenic proliferation and migration of endothelial cells, resulting in
 CC formation of new capillaries and collateral vessels to help restore
 CC function to damaged or ischaemic heart tissue. The present sequence
 CC represents a thrombin derivative peptide of the invention.
 XX
 SQ Sequence 4 AA;
 CC
 DR 03-OCT-2002 (revised)
 DT 22-JUN-1991 (first entry)
 XX
 DE Sequence of peptide with the same cell-attachment-promoting activity as
 DE fibronectin.
 XX
 SQ Sequence 9
 CC
 DR AAP6125 standard; peptide; 4 AA.
 ID AAP6125;
 XX
 AC AAP6125;
 XX
 DT 03-OCT-2002 (revised)
 DT 22-JUN-1991 (first entry)
 XX
 DE Sequence of peptide with the same cell-attachment-promoting activity as
 DE fibronectin.
 XX
 SQ Sequence 8
 CC
 DR Cell attachment; phagocytosis; injury therapy.
 ID ABB80263 standard; peptide; 4 AA.
 XX
 AC ABB80263;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Misc-difference 1

XX Cyclic peptide; cell contact inhibitor; hydrolytic enzyme.
 XX Synthetic.

XX PH Location/Qualifiers
 PT Modified-site 2
 /label= MeGly

XX JPO426407-A.
 PN 18-SEP-1992.
 XX 16-FEB-1991; 91JP-00044386.
 PR 16-FEB-1991; 91JP-00044386.
 PA (ASAG) ASAHI GLASS CO LTD.
 DR WPI; 1992-361922/44.

XX Peptide derivs. as contact inhibitor for animal cells - comprise synthesised cyclic peptide and have portion of aminoacid sequence of PT arginine-N-methyl-glycine-aspartic acid.

PS Disclosure; Page 3; 6PP; Japanese.

XX The sequences Given in AAR25311-19 are cyclic peptides which act as contact inhibitors of animal cells. They are resistant to decomposition by hydrolytic enzymes and can be maintained at high levels of activity for a long period in vivo. The peptides are cyclic and may have 1-16 CC pref. 1-4 amino acids

XX SQ Sequence 4 AA;

Query Match 81.7%; Score 18; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 14
 AAR26806
 ID AAR26806 standard; peptide; 4 AA.
 AC AAR26806;
 XX 12-FEB-1993 (first entry)
 DT XX
 DE Propen-amido peptide copolymer.
 KW Tumour metastasis inhibitor; platelet aggregation; animal cell; adhesion; wound healing; cell culture media.

XX OS Synthetic.

XX Key
 FT Modified-site 1
 /note= "CH₂=CH-CO-NH-(CH₂)₃-CO-Arg"
 FT XX
 JP04213311-A.
 FN XX
 PD 04-AUG-1992.
 XX PP 29-MAR-1991; 91JP-00066159.
 XX PR 27-NOV-1990; 90JP-00324610.
 XX FA (FUJIF) FUJI PHOTO FILM CO LTD.
 XX WPI; 1992-305482/37.
 XX New copolymers of propen-amido peptide(s) - are tumour metastasis, platelet aggregation and animal cell adhesion inhibitors also useful as wound healing agents and cell culture media. See also AAR26805-R26808
 XX SQ Sequence 4 AA;

RESULT 13
 AAR26810
 ID AAR26810 standard; peptide; 4 AA.
 AC AAR26810
 XX 20-MAY-1998 (first entry)
 DT XX
 DE Polyethylene glycol derivative #1.
 XX triazine ring; methoxy-polyethyleneoxy group; fibronectin; vironectin; platelet adhesion; metastasis; neuropathy.
 XX Synthetic.
 XX JP04217693-A.
 XX 07-AUG-1992.
 XX 30-NOV-1990; 90JP-00333717.
 PR 23-OCT-1990; 90JP-00285172.
 XX PA (FUJIF) FUJI PHOTO FILM CO LTD.
 XX DR 1992-312284/38.
 PR XX
 PT Polyethylene glycol derivs. contg. peptide(s) - inhibit cellular adhesion or for fibronectin or vironectin and are used to inhibit agglutination or

BT adhesion of platelets.
 XX Disclosure; Page 3; 9PP; Japanese.
 XX The sequences given in AAR26810-14 are examples of a peptide chain which is attached once or twice to a triazine ring which is also substituted twice or once, respectively, with a methoxy-polyethyleneoxy group. These peptides can be used to inhibit cellular adhesion to fibronectin or vironectin and they are useful as inhibitors for agglutination or adhesion of platelets. They can also be useful as inhibitors for metastasis of cancers, inhibitors of agglutination of platelets caused by tumour cells in the blood capillaries, and drugs acting on neuropathy

XX SQ Sequence 4 AA;

Query Match 85.7%; Score 18; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

Db 1 |||:
 1 RGDS 4

RESULT 15
 AAR26398 standard; peptide; 4 AA.
 ID AAR26398
 XX
 AC AAR26398;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JAN-1993 (first entry)
 XX
 DE Sequence of platelet binding peptide.
 XX
 KW Technetium-99m labelled polypeptide imaging agent; radiolabeled imaging;
 KW
 Radiodiagnostic agent.
 OS
 Synthetic.
 XX
 PN WO9213572-A1.
 XX
 PD 20-AUG-1992.
 XX
 PF 92WO-US000757.
 XX
 PR 07-FEB-1992;
 PR 08-FEB-1991;
 PR 91US-00653012.
 XX
 PA (DIAT-) DATECH INC.
 XX
 PI
 Dean RT;
 XX
 DR 1992-299767/36.
 XX
 PT New technetium-99m labelled polypeptide imaging agents - for imaging of
 PT clots, tumours, infection sites, atherosclerotic and amyloid plaques or
 PT bone, and for visualising organs.
 XX
 PS Page 13; 19pp; English.
 XX
 CC The binding peptide is covalently linked to a 'Cp(aa)Cp' technetium
 CC binding group wherein Cp is a protected cysteine and (aa) is an amino
 CC acid. The technetium-99m complexes are used to image target sites within
 CC a mammalian body. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

Query Match	85.7%	Score 18;	DB 2;	Length 4;
Best Local Similarity	75.0%	Prd. No.	1.4e+06;	
Matches	3;	Conservative	1;	Mismatches 0;
				Indels 0;
Gaps	0;			

Qy 1 RGDA 4
 1 |||:
 Db 1 RGDS 4

Search completed: February 26, 2004, 09:33:05
 Job time : 54 secs

Copyright GenCore version 5.1.6
 (c) 1993 - 2004 Compugen Ltd.
 protein search, using sw model
 run on: February 26, 2004, 09:34:21 ; Search time 32 Seconds
 (without alignments)
 scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5
 title: US-09-909-348-3
 effect score: 21 RgDA 4
 sequence: 1 RgDA 4
 searched: 809742 seqs, 21113259 residues
 total number of hits satisfying chosen parameters: 5110
 post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries
 Published Applications AA:
 1: /cgn2_6/prodata/2/pubpaas/us07_pubcomb.pep: *
 2: /cgn2_6/prodata/2/pubpaas/fct_new_pub.pep: *
 3: /cgn2_6/prodata/2/pubpaas/us06_pubcomb.pep: *
 4: /cgn2_6/prodata/2/pubpaas/us06_pubcomb.pep: *
 5: /cgn2_6/prodata/2/pubpaas/us07_pub.pep: *
 6: /cgn2_6/prodata/2/pubpaas/pctos_pubcomb.pep: *
 7: /cgn2_6/prodata/2/pubpaas/us08_new_pub.pep: *
 8: /cgn2_6/prodata/2/pubpaas/us08_pubcomb.pep: *
 9: /cgn2_6/prodata/2/pubpaas/us09_pubcomb.pep: *
 10: /cgn2_6/prodata/2/pubpaas/us09c_pubcomb.pep: *
 11: /cgn2_6/prodata/2/pubpaas/us09c_pubcomb.pep: *
 12: /cgn2_6/prodata/2/pubpaas/us09c_new_pub.pep: *
 13: /cgn2_6/prodata/2/pubpaas/us10_pubcomb.pep: *
 14: /cgn2_6/prodata/2/pubpaas/us10c_pubcomb.pep: *
 15: /cgn2_6/prodata/2/pubpaas/us10c_pubcomb.pep: *
 16: /cgn2_6/prodata/2/pubpaas/us10c_new_pub.pep: *
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 18: /cgn2_6/prodata/2/pubpaas/us60_pubcomb.pep: *
 RESULT 1
 US-09-909-348-3
 : Sequence 3, Application US/09909348
 ; Patent No. US000042373A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carney, Darrell H.
 ; APPLICANT: Crowther, Roger S.
 ; APPLICANT: Bergmann, John
 ; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
 ; TITLE OF INVENTION: For The No. US20020042373A1-Proteolytically Activated Thrombin
 ; FILE REFERENCE: 3033.1003-001
 ; CURRENT APPLICATION NUMBER: US/09/909,348
 ; CURRENT FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: US 60/219,800
 ; PRIOR FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastaBE for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-348-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES
 % Query Match Length DB ID Description
 Result No. Score

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	4	9	US-09-909-348-3	Sequence 3, Appli
2	21	100.0	4	9	US-09-904-090-1	Sequence 1, Appli
3	21	100.0	4	9	US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4	10	US-09-911-569-23	Sequence 23, Appli
5	21	100.0	4	13	US-10-050-632-3	Sequence 1, Appli
6	21	100.0	4	13	US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4	13	US-10-050-688-3	Sequence 3, Appli
8	21	100.0	4	14	US-10-200-879-23	Sequence 6, Appli
9	18	85.7	4	9	US-09-823-447-6	Sequence 9, Appli
10	18	85.7	4	9	US-09-010-714-9	Sequence 21, Appli
11	18	85.7	4	9	US-09-945-715-21	Sequence 1, Appli
12	18	85.7	4	9	US-09-935-168-1	Sequence 5, Appli
13	18	85.7	4	9	US-09-942-117-5	Sequence 23, Appli
14	18	85.7	4	10	US-09-911-560-22	Sequence 23, Appli
15	18	85.7	4	11	US-09-991-558-23	Sequence 1, Application US/09904090-1

Patent No. US20020061852A1
 GENERAL INFORMATION:
 TITLE OF INVENTION: PEPTIDES
 FILE REFERENCE: 3033.1.000-001
 CURRENT APPLICATION NUMBER: US/09/904,090
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: US 60/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 4
 FEATURE:
 OTHER INFORMATION: Polypeptide, fragment of thrombin
 ORGANISM: Artificial Sequence
 US-09-904-090-1
 Query Match Similarity 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.2e-05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 3
 US-09-909-122-3
 / Sequence 3, Application US/09909122
 / Patent No. US2002012620A1
 / GENERAL INFORMATION:
 / APPLICANT: Carney, Darrell H.
 / APPLICANT: Crowther, Roger S.
 / APPLICANT: Simmons, David J.
 / APPLICANT: Yang, Jinping
 / APPLICANT: Redin, William R.
 / TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 / FILE REFERENCE: 3033.1.002-001
 / CURRENT APPLICATION NUMBER: US/09/909,122
 / CURRENT FILING DATE: 2001-07-19
 / PRIOR APPLICATION NUMBER: US 60/219,300
 / PRIOR FILING DATE: 2000-07-19
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 3
 / LENGTH: 4
 / FEATURE:
 / OTHER INFORMATION: Peptide fragment of Thrombin
 / US-09-909-122-3
 Query Match Similarity 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.2e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 4
 US-09-911-569-23
 / Sequence 23, Application US/09911569
 / Publication No. US2003006917A1
 / GENERAL INFORMATION:
 / APPLICANT: Hawley-Nelson, Pamela
 / APPLICANT: Lan, Jianqiang
 / APPLICANT: Shih, Pojen
 / NUMBER OF SEQ ID NOS: 6
 / SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 3
 LENGTH: 4
 TYPE: PRT
 FEATURE:
 OTHER INFORMATION: Fragment of human prothrombin
 US-10-050-692-3

Query Match	100.0%	Score 21;	DB 13;	Length 4;
Best Local Similarity	100.0%	Pred. No.	7.2e+05;	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Qy	1 RGDA 4			
Db	1 RGDA 4			

RESULT 6
 US-10-050-611-1
 Sequence 1, Application US/10050611
 PUBLICATION NUMBER: US20020187933A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
 CURRENT APPLICATION NUMBER: US/10/050,611
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/904,090
 PRIOR FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 60/217,583
 PRIOR FILING DATE: 2000-07-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: human fragment of thrombin
 US-10-050-611-1

Query Match	100.0%	Score 21;	DB 13;	Length 4;
Best Local Similarity	100.0%	Pred. No.	7.2e+05;	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Qy	1 RGDA 4			
Db	1 RGDA 4			

RESULT 7
 US-10-050-688-3
 Sequence 3, Application US/10050688
 PUBLICATION NUMBER: US20020198154A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Stemberg, Janet
 APPLICANT: Bergmann, John
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
 TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
 FILE REFERENCE: 2033_1103-004
 CURRENT APPLICATION NUMBER: US/10/050,688
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,348
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,800
 PRIOR FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3

LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of thrombin
 US-10-050-688-3

Query Match	100.0%	Score 21;	DB 13;	Length 4;
Best Local Similarity	100.0%	Pred. No.	7.2e+05;	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Qy	1 RGDA 4			
Db	1 RGDA 4			

RESULT 8
 US-10-200-879-23
 Sequence 23, Application US/10200879
 Publication No. US0030144230A1
 GENERAL INFORMATION:
 APPLICANT: Hawley-Nelson, Pamela
 LAN, JIANQING
 SHIH, POSEN
 JESSE, JOEL A.
 SCHIFFERL, KEVIN P.
 GEBREHU, GUILLAT
 TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSECTIONS
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GREENLEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/200,879
 FILING DATE: 23-Jul-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/911,569
 FILING DATE: 23-JUL-2001
 APPLICATION NUMBER: US 09/039,780
 FILING DATE: 16-MAR-1998
 APPLICATION NUMBER: US 08/818,200
 FILING DATE: 14-MAR-1997
 APPLICATION NUMBER: US 08/658,130
 FILING DATE: 04-JUN-1996
 APPLICATION NUMBER: US 08/477,354
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: SULLIVAN, SALLY A.
 REGISTRATION NUMBER: 32,064
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-200-879-23

Query Match Score 21; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 9

US-09-823-444-6
 Sequence 6, Application US/09823444
 Patent No. US200200953A1
 GENERAL INFORMATION:
 APPLICANT: Bednar, Bohumil
 INVENTION: Bollaq, Daniel M.
 APPLICANT: Gould, Robert J.
 APPLICANT: Merck & Co., Inc.
 TITLE OF INVENTION: ANTICOAGULANT TEST
 FILE REFERENCE: 19100
 CURRENT APPLICATION NUMBER: US/09/B23,444
 CURRENT FILING DATE: 2001-03-10
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

OTHER INFORMATION: This sequence is a synthetically prepared peptide.

US-09-823-444-6

Query Match Score 18; DB 9; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 10

US-09-010-714-9
 Sequence 9, Application US/09010714
 Patent No. US20020012942A1
 GENERAL INFORMATION:
 APPLICANT: McCarthy, James B.
 APPLICANT: Furcht, Leo T.
 APPLICANT: Iida, Joji
 TITLE OF INVENTION: POLYPEPTIDES WITH ALPHAI 4 INTEGRIN SUBUNIT RELATED
 FILE REFERENCE: 600-332US01
 CURRENT APPLICATION NUMBER: US/09/010,714
 CURRENT FILING DATE: 1998-01-22
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 9
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-010-714-9

Query Match Score 18; DB 9; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7.2e+05;
 Matches 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 11

US-09-925-715-21
 Sequence 21, Application US/09925715
 Patent No. US2002010221A1
 GENERAL INFORMATION:
 APPLICANT: Nycomed Imaging AS
 TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
 FILE REFERENCE: REF/Klavens/206
 CURRENT APPLICATION NUMBER: US/09/925,715
 CURRENT FILING DATE: 2001-08-10
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 21
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic RGDS
 OTHER INFORMATION: Sequence
 US-09-925-715-21

Query Match Score 18; DB 9; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 12

US-09-935-168-1
 Sequence 1, Application US/09935168
 Patent No. US2002010673A1
 GENERAL INFORMATION:
 APPLICANT: West, Jennifer L.
 APPLICANT: Mann, Brenda K.
 TITLE OF INVENTION: Tissue Engineering Scaffolds Promoting Matrix Protein Production
 CURRENT APPLICATION NUMBER: US/09/935,168
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:
 OTHER INFORMATION: cell adhesion ligand
 US-09-935-168-1

Query Match Score 18; DB 9; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 13

US-09-042-117-5
 Sequence 5, Application US/09942117
 Publication No. US2002019770A1
 GENERAL INFORMATION:
 APPLICANT: Menrad, Andreas
 APPLICANT: Redlitz, Alexander
 APPLICANT: Kopplitz, Marcus
 APPLICANT: Egner, Ursula
 APPLICANT: Bahr, Inke
 TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
 FILE REFERENCE: SCH-1832

CURRENT APPLICATION NUMBER: US/09/942,117
 CURRENT FILING DATE: 2002-06-24
 PRIOR FILING DATE: DE 10045803.3
 PRIOR APPLICATION NUMBER: DE 1000-09-07
 PRIOR FILING DATE: 2000-09-07
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 5
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-942-117-5

Query Match 85.7%; Score 18; DB 9; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 14
 US-09-911-569-22
 Sequence 22, Application US/09911569
 Publication No. US2003006173A1
 GENERAL INFORMATION:
 APPLICANT: HAWLEY-NELSON, PAMELA
 LAN, JIANGQING
 SHIH, POJEN
 JESSE, JOEL A.
 SCHIFFERLI, KEVIN P.
 GEBEYEHU, GULILAT
 TITLE OF INVENTION: PEPTIDE ENHANCED TRANSFECTIONS
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: GREENLEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/911,569
 FILING DATE: 23-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/039,780
 FILING DATE: 16-MAR-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: SULLIVAN, SALLY A.
 REGISTRATION NUMBER: 32,064
 REFERENCE/DOCKET NUMBER: 32-95D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303)499-8089
 TELEFAX: (303)499-8089
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO

ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-911-569-22

Query Match 85.7%; Score 18; DB 10; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 15
 US-09-991-568B-23
 Sequence 23, Application US/09991568B
 Publication No. US20030219429A1
 GENERAL INFORMATION:
 APPLICANT: Buddy, John A.
 TITLE OF INVENTION: Composition and Method for Bone Regeneration
 FILE REFERENCE: 1008-120-US
 CURRENT APPLICATION NUMBER: US/09/991,568B
 CURRENT FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 09/122,348
 PRIOR FILING DATE: 1998-07-24
 NUMBER OF SEQ ID NOS: 23
 SEQ ID NO: 23

LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Purchased commercially or sequence is synthesized
 US-09-991-568B-23

Query Match 85.7%; Score 18; DB 11; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7.2e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

Search completed: February 26, 2004, 09:39:36
 Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:32:06 ; Search time 23 Seconds
(without alignments)

BLOSUM62

Scoring table: Gapext 0.5
Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 9930

Minimum DB seq length: 4
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Parents AA:
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2: /cgnd_6_ptodata/2/iaa/5B_COMB.pep:
3: /cgnd_6_ptodata/2/iaa/6A_COMB.pep:
4: /cgnd_6_ptodata/2/iaa/6B_COMB.pep:
5: /cgnd_6_ptodata/2/iaa/PC10S_COMB.pep:
6: /cgnd_6_ptodata/2/iaa/backfile1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	4	1	US-08-658-130-19	Sequence 19, Appli
2	21	100.0	4	4	US-08-039-7804-23	Sequence 23, Appli
3	21	100.0	4	4	US-08-538-504-1	Sequence 1, Appli
4	21	100.0	4	4	US-09-631-137C-1	Sequence 1, Appli
5	21	100.0	4	5	PCT-US96-08723-19	Sequence 19, Appli
6	21	100.0	4	6	5352664-2	Patent No. 5352664
7	18	85.7	4	1	US-07-780-790A-7	Sequence 7, Appli
8	18	85.7	4	1	US-07-683-957B-7	Sequence 7, Appli
9	18	85.7	4	1	US-07-834-848-16	Sequence 16, Appli
10	18	85.7	4	1	US-08-127-351-54	Sequence 16, Appli
11	18	85.7	4	1	US-08-109-106-1	Sequence 1, Appli
12	18	85.7	4	1	US-08-251-027-8	Sequence 8, Appli
13	18	85.7	4	1	US-08-480-367B-54	Sequence 54, Appli
14	18	85.7	4	1	US-08-487-221A-54	Sequence 54, Appli
15	18	85.7	4	1	US-08-480-370-54	Sequence 54, Appli
16	18	85.7	4	1	US-08-389-005-1	Sequence 1, Appli
17	18	85.7	4	1	US-08-178-482-11	Sequence 11, Appli
18	18	85.7	4	1	US-08-299-636-35	Sequence 35, Appli
19	18	85.7	4	1	US-08-729-155-24	Sequence 34, Appli
20	18	85.7	4	1	US-08-142-49B-13	Sequence 13, Appli
21	18	85.7	4	1	US-08-464-456-33	Sequence 33, Appli
22	18	85.7	4	1	US-08-128-225-2	Sequence 2, Appli
23	18	85.7	4	1	US-08-405-200-1	Sequence 1, Appli
24	18	85.7	4	1	US-08-596-116A-67	Sequence 67, Appli
25	18	85.7	4	1	US-08-596-116A-70	Sequence 70, Appli
26	18	85.7	4	1	US-08-338-282-12	Sequence 12, Appli
27	18	85.7	4	1	US-08-658-130-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-658-130-19
; Sequence 19, Application US/08658130
; Parent No. 5736392
; GENERAL INFORMATION:
; APPLICANT: Hawley-Nelson, Pamela
; APPLICANT: Lan, Jiangang
; APPLICANT: Shih, Pojen
; APPLICANT: Jesse, Joel A.
; APPLICANT: Shiffner, Kevin P.
; TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
; TITLE OF INVENTION: Transfections
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenberg, Winner and Sullivan, P.C.
; STREET: 570 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658.130
; FILING DATE: 04-JUN-1995
; CLASIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,354
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carrthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 32-95A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; FRAGMENT TYPE: internal
; US-08-658-130-19

Query Match Similarity 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 2

US-09-039-780A-23
 Sequence 23 Application US/09039780A

Patent No. 6375248

GENERAL INFORMATION:
 ADDRESS: HAWLEY-NELSON, PAMELA

LAN, JIANGQING SHIH, POJEN

JESS, JOEL A. SCHIFFERLI, KEVIN P.

GEBEYEHU, GUILLAT

TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:

ADDRESS: GREENLEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO

Country: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Patent In Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/039,780A

FILING DATE: 16-Mar-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: SULLIVAN, SALLY A.

REGISTRATION NUMBER: 32,064

TELECOMMUNICATION INFORMATION: 32-95C

TELEPHONE: (303) 439-8080

TELEFAX: (303) 439-8089

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 4

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE: RGDA

TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES:
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P O Box 4433
 CITY: Houston
 STATE: Texas
 COUNTY: U.S.A.
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/538,504
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Parker, David L.
 REGISTRATION NUMBER: 32,165
 REFERENCE/DOCKET NUMBER: UTSG:178/PAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-538-504-1

Query Match Similarity 100.0%; Score 21; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 4

US-09-631-137C-1

Sequence 1, Application US/09631137C
 Patent No. 6630512

GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.

APPLICANT: Glein, Kevin C.

TITLE OF INVENTION: Thrombin Derived Polypeptides:
 Compositions and Methods for Use

FILE REFERENCE: 3033-1001-004

CURRENT APPLICATION NUMBER: US/09/631,137C
 CURRENT FILING DATE: 2000-08-07
 PRIOR APPLICATION NUMBER: US 08/538,504
 PRIOR FILING DATE: 1995-09-29
 PRIOR APPLICATION NUMBER: US 08/007,173
 PRIOR FILING DATE: 1993-01-21
 PRIOR APPLICATION NUMBER: US 06/925,201
 PRIOR FILING DATE: 1986-10-31
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fragment of human prothrombin

US-09-631-137C-1

Query Match Similarity 100.0%; Score 21; DB 4; Length 4;

Qy 1 RGDA 4
 Db 1 RGDA 4

RESULT 3

US-08-538-504-1

Sequence 1, Application US/08538504
 Patent No. 6627731

GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Glein, Kevin C.

Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0; LENGTH: 4;
 Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 PCT-US96-08723-19
 Sequence 19, Application PC/TUS9608723
 GENERAL INFORMATION:
 APPLICANT: Life Technologies, Inc.
 TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 STREET: 5310 Manhattan Circle, Suite 201
 CITY: Boulder
 STATE: Colorado
 ZIP: 80303 US
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/08723
 FILING DATE: 04-JUN-1996
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/477,354
 ATTORNEY/AGENT INFORMATION:
 NAME: Caruthers, Jennie M.
 REGISTRATION NUMBER: 34,464
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-9880
 TELEFAX: (303) 499-8099
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 PCT-US96-08723-19
 Query Match 100.0%; Score 21; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 PCT-US96-08723-19
 Sequence 19, Application PC/TUS9608723
 GENERAL INFORMATION:
 APPLICANT: Goldstein, Michael J.
 TITLE OF INVENTION: Polypeptides Comprising a Conserved Internal Region
 NUMBER OF SEQUENCES: 3
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/477,354
 FILING DATE: 04-JUN-1996
 SEQ ID NO: 21

RESULT 7
 US-07-780-790A-7
 Sequence 7, Application US/07780790A
 GENERAL INFORMATION:
 APPLICANT: Kojima, Masayoshi
 APPLICANT: Komazawa, Hiroyuki
 TITLE OF INVENTION: CM-CHITIN DERIVATIVES AND USE THEREOF
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sugihara, Mion, Zinn, Macpeak, & Seas
 STREET: 2100 Pennsylvania Avenue
 CITY: Washington
 STATE: District of Columbia
 COUNTRY: USA
 ZIP: 20037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/780,790A
 FILING DATE: 19911023
 CLASSIFICATION: 530
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7060
 TELEFAX: (202)293-7860
 TELEX: 6491103
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-780-790A-7

Query Match 85.7%; Score 18; DB 1; Length 4;
 Best Local Similarity 75.0%; Pred. No. 3e+05; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 US-07-683-957B-7
 Sequence 7, Application US/07683957B
 GENERAL INFORMATION:
 APPLICANT: Donahoe, Patricia K.
 APPLICANT: Radin, Richard C.
 APPLICANT: MacLaughlin, David T.
 TITLE OF INVENTION: Purification of Mllerian Inhibiting Substance
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington

STATE: D.C.
 COUNTY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/683,957B
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldstein, Jorge A.
 REGISTRATION NUMBER: 29,041
 REFERENCE/DOCKET NUMBER: 0609-3060000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 466-0800
 TELEX/FAX: (202) 833-8716
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-834-848-16

RESULT 9
 US-07-834-848-16
 / Sequence 16, Application US/07834848
 / Patent No. 5436221
 / GENERAL INFORMATION:
 / APPLICANT: KITAGUCHI, HIROSHI
 / APPLICANT: KONAZAWA, HIROYUKI
 / APPLICANT: KOJIMA, MASAYOSHI
 / APPLICANT: MOGI, HIDETO
 / APPLICANT: NISHIKAWA, NAOYUKI
 / APPLICANT: SATOH, HIDEAKI
 / APPLICANT: Orikasa, Atsushi
 / APPLICANT: Ono, MITSUNORI
 / APPLICANT: AZUMA, ICHIRO
 / APPLICANT: SAKAI, IKUO
 / TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION
 / NUMBER OF SEQUENCES: 18
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Sugihara, Mion, Macpeak, & Seas
 / STREET: 2100 Pennsylvania Ave., NW
 / CITY: Washington
 / STATE: DC
 / COUNTRY: USA
 / ZIP: 20037-1202
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/07/834,848
 / FILING DATE: 1992/2/13
 / CLASSEMENT: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Biggart, Waddell A.
 / REGISTRATION NUMBER: 24,861

RESULT 10
 US-08-127-351-34
 / Sequence 54, Application US/08127351
 / Patent No. 54,49761
 / GENERAL INFORMATION:
 / APPLICANT: BELINKA, JR., BENJAMIN A.
 / APPLICANT: COUGHLIN, DANIEL J.
 / APPLICANT: ALVAREZ, VERNON L.
 / APPLICANT: WOOD, RICHARD
 / TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
 / NUMBER OF SEQUENCES: 56
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER &
 / ADDRESSEE: NEUSTADT,
 / ADDRESSEE: P. C.
 / STREET: 1755 S. Jefferson Davis Highway, Suite 400
 / CITY: Arlington
 / STATE: Virginia
 / COUNTRY: U.S.A.
 / ZIP: 22202
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/127,351
 / FILING DATE: 28-SEP-1993
 / CLASSIFICATION: 534
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Villacorta, Gilberto M.
 / REGISTRATION NUMBER: 34,038
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Neustadt, Daniel J.
 / STREET: 1755 S. Jefferson Davis Highway, Suite 400
 / CITY: Arlington
 / STATE: Virginia
 / COUNTRY: U.S.A.
 / ZIP: 22202
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/127,351
 / FILING DATE: 28-SEP-1993
 / CLASSIFICATION: 534
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Villacorta, Gilberto M.
 / REGISTRATION NUMBER: 34,038
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Neustadt, Daniel J.
 / STREET: 1755 S. Jefferson Davis Highway, Suite 400
 / CITY: Arlington
 / STATE: Virginia
 / COUNTRY: U.S.A.
 / ZIP: 22202
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/07/834,848
 / FILING DATE: 1992/2/13
 / CLASSEMENT: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Biggart, Waddell A.
 / REGISTRATION NUMBER: 24,861

RESULT 18
 US-08-127-351-54
 / Sequence 18, Application US/08127351
 / Best Local Similarity 75.0%; Pred. No. 3e+05;
 / Matches 3; Conservative 1; Mismatches 0; Indels 0;
 / Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 18
 US-08-127-351-54
 / Sequence 18, Application US/08127351
 / Best Local Similarity 75.0%; Pred. No. 3e+05;
 / Matches 3; Conservative 1; Mismatches 0; Indels 0;
 / Gaps 0;

Qy 1 RGDA 4

|||:
Db 1 RGDS 4

RESULT 11
US-08-109-106-1
Sequence 1, Application US/08109106
Patent No. 5475100
GENERAL INFORMATION:
APPLICANT: Kimikazu HASHINO et al.
TITLE OF INVENTION: Artificial Antibody
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEES: Wendoroth, Lind & Ponack #700
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
APPLICATION NUMBER: US/08/109,106
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/725, 668
FILING DATE: July 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
SEQUENCE FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:

RESULT 12
US-08-251-027-8
Sequence 8, Application US/08251027
Patent No. 5519005
GENERAL INFORMATION:
APPLICANT: Lider, Ofer
APPLICANT: Greenspoon, Ram
APPLICANT: Hershkoiz, Ram
APPLICANT: Alon, Ronen
TITLE OF INVENTION: A METHOD OF INHIBITION OF CELLULAR AND MOLECULAR LEVEL BIOLOGICAL INTERACTIONS UTILIZING NON-PEPTIDIC SURROGATES OF THE ARG-GLY-ASP SEQUENCE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5519005thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,027
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDS 4

RESULT 13
US-08-480-367B-54
Sequence 54, Application US/08480367B
Patent No. 557888

GENERAL INFORMATION:
 APPLICANT: BELINKA JR, BENJAMIN A.
 APPLICANT: COUGHLIN, DANIEL J.
 APPLICANT: ALVAREZ, VERNON L.
 APPLICANT: WOOD, RICHARD

TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
 NUMBER OF SEQUENCES: 56

ATTORNEY/AGENT INFORMATION:
 ADDRESS: LOWE PRICE LeBLANC & BECKER
 STREET: 99 Canal Center Plaza, Suite 300
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: U.S.A.

ZIP: 22314

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 REFERENCE/DOCKET NUMBER: 2654-002A

APPLICATION NUMBER: US/08/480,367B
 FILING DATE: 07-06-95
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Villacorta, Gilberto M.
 REGISTRATION NUMBER: 34,018
 REFERENCE/DOCKET NUMBER: 07-1995

TELEPHONE: (703) 684-1111
 TELEX:

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

US-08-480-367B-54

Query Match Score 18; DB 1; Length 4;
 Best Local Similarity 75.0%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 14
US-08-487-221A-54
Sequence 54, Application US/08487221A
Patent No. 5593656

GENERAL INFORMATION:
 APPLICANT: BELINKA JR, BENJAMIN A.
 APPLICANT: COUGHLIN, DANIEL J.
 APPLICANT: ALVAREZ, VERNON L.
 APPLICANT: WOOD, RICHARD

TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
 NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAYER &
 ADDRESS: NEUSTADT, P.C.
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.

RESULT 15
US-08-480-370-54
Sequence 54, Application US/08480370
Patent No. 5609847

GENERAL INFORMATION:
 APPLICANT: BELINKA JR, BENJAMIN A.
 APPLICANT: COUGHLIN, DANIEL J.
 APPLICANT: ALVAREZ, VERNON L.
 APPLICANT: WOOD, RICHARD

TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
 NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAYER &
 ADDRESS: NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,370
 FILING DATE:
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/127,351
 FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Villacorta, Gilberto M.

REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
4 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-480-370-54

Query Match Score 18; DB 1; Length 4;
Best Local Similarity 85.7%; Score 18;
Matches 3; Pred. No. 3e05; Mismatches 0;
Matches 3; Conservative 1; Indels 0; Gaps 0;
QY 1 RGDA 4
Db 1 RGDS 4

Search completed: February 26, 2004, 09:35:27
Job time : 24 secs

RESULT 3
 PH0321
 Ig heavy chain DJ region (clone C72-96R) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1321
 R;Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A;Reference number: PMID:1460419
 A;Accession: PH1321
 A;Molecule type: DNA
 A;Residues: 1-14 <WAS>
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 20; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 3.7e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACXGDSG 10
 Db 4 SCLGATG 10

RESULT 4
 S23376
 collagen alpha chain - polychaete (*Alvinella pompejana*) (fragment)
 C;Species: Alvinella pompejana
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-May-1998
 R;Gail, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.
 J. Mol. Biol. 221, 209-223, 1991
 A;Title: Molecular characterization of cuticle and interstitial collagens from worms col
 A;Reference number: S17581; MUID:92015295; PMID:1920405
 A;Accession: S23376
 A;Molecule type: protein
 A;Residues: 1-14 <GAI>

Query Match Score 19; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GGP 12
 Db 5 GGP 7

RESULT 5
 PH0747
 T-cell receptor beta chain (M1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: PH0747
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:1836010
 A;Accession: PH0747
 A;Molecule type: mRNA
 A;Residues: 1-14 <CAS>
 A;Cross-references: EMBL:X60818
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match Score 19; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 5.4e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CXGDSGG 11
 Db 1 CAWGTTGG 7

RESULT 6
 S36692
 ribosomal protein - Mycobacterium bovis (fragment)
 C;Species: Mycobacterium bovis
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C;Accession: S36692
 R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac
 A;Reference number: S36692
 A;Accession: S36692
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <CHA>

Query Match Score 17; DB 2; Length 14;
 Best Local Similarity 33.3%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 3 DACKGDSGGPVX 14
 Db 2 EAETGAKAKAPRV 13

RESULT 7
 S09721
 2S albumin small chain nIII - rape (fragments)
 C;Species: Brassica napus (rape)
 C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
 C;Accession: S09721
 R;Monsalve, R.I.; Mendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
 FEBS Lett. 263, 209-212, 1990
 A;Title: Beta-turns as structural motifs for the proteolytic processing of seed proteins
 A;Reference number: S9720; MUID:90242974; PMID:2185951
 A;Accession: S09721
 A;Molecule type: protein
 A;Residues: 1-9;10-14 <MON>
 A;Experimental source: seed
 A;Keywords: 2S albumin

Query Match Score 17; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 SGCP 12
 Db 1 SAGP 4

RESULT 8
 PH0776
 T-cell receptor alpha chain (M1 v-alpha-8.F3.3) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: PH0776
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:92078846; PMID:1836010
 A;Accession: PH0776
 A;Molecule type: mRNA
 A;Residues: 1-14 <CAS>
 A;Cross-references: EMBL:X60873
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match Score 17; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CXGDSGG 11
 Db :|||

Db 1 CALGTGG 7 Query Match Score 16; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
RESULT 9

PHO765 T-cell receptor beta chain (H1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C;Accession: PHO765
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J;Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I
 allelic exclusion and antigen-specific repertoire.
 A;Reference number: PHO746; MUID:92078846; PMID:1836010
 A;Accession type: mRNA
 A;Residues: 1-14 <CAS>
 A;Cross-references: EMBL:X60859; NID:951139; PIDN:CAA43249.1; PID:951140
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match Score 17; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 RGD 3 Query Match Score 16; DB 2; Length 14;
 Db 7 RGD 9 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 10

PHO755 T-cell receptor beta chain (QAL1.3.2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C;Accession: PHO755
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J;Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I
 allelic exclusion and antigen-specific repertoire.
 A;Reference number: PHO746; MUID:92078846; PMID:1836010
 A;Accession type: mRNA
 A;Residues: 1-14 <CAS>
 A;Cross-references: EMBL:X60849; NID:953876; PIDN:CAA43240.1; PID:953877
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match Score 17; DB 2; Length 14;
 Best Local Similarity 37.5%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 5;
 Indels 0; Gaps 0;

Qy 5 CXGDSGGP 12 Query Match Score 16; DB 2; Length 14;
 Db 1 CASRDCQP 8 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

RESULT 11

B29743 Translation initiation factor eIF-2 alpha chain-associated kinase phosphopeptide - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Oct-1997
 C;Accession: B29743
 R;Rose, D.W.; Wettenhall, R.E.H.; Kudlicki, W.; Kramer, G.; Hardisty, B.
 Biochemistry 26, 6583-6587, 1987
 A;Title: The 90-kilodalton peptide of the heme-regulated eIF-2-alpha kinase has sequence
 A;Reference number: A90321; MUID:88107571; PMID:342708
 A;Accession: B29743
 A;Molecule type: protein
 A;Residues: 1-14 <ROS>
 A;Experimental source: reticulocyte
 C;Superfamily: heat shock protein 90

RESULT 12

PT0232 Ig heavy chain CRD3 region (clone 1-124) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0232
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J;Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity by the human Ig heavy chain CRD3 region.
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0232
 A;Molecule type: DNA
 A;Residues: 1-14 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 16; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

Qy 8 DSGG 11 Query Match Score 16; DB 2; Length 14;
 Db 6 DSSG 9 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

RESULT 13

PT0252 Ig heavy chain CRD3 region (clone 2-109D) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0252
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J;Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity by the human Ig heavy chain CRD3 region.
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0252
 A;Molecule type: DNA
 A;Residues: 1-14 <ZAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 16; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

Qy 8 DSGG 11 Query Match Score 16; DB 2; Length 14;
 Db 7 DSSG 10 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

RESULT 14

PT0254 Ig heavy chain CRD3 region (clone 2-115A) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0254
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J;Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity by the human Ig heavy chain CRD3 region.
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0254
 A;Molecule type: DNA
 A;Residues: 1-14 <ZAM>
 A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match Similarity 22.5%; Score 16; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 DSGG 11
 Db 8 DSSG 11

RESULT 15

S47366 T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-an-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47366

R;Lechner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47355

A;Accession: S47366

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 114 <LEH>

A;Cross-references: EMBL:235691; NID:9527473; PIDN:CAA84760.1; PID:9527474

C;Keywords: T-cell receptor

Query Match Similarity 22.5%; Score 16; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 1.7e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 5 CXGDSGG 11
 Db 3 CRG-GG 7

Search completed: February 26, 2004, 09:41:38
 Job time : 22 secs

Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	
Searched:	141681 seqs, 52070155 residues		
Total number of hits satisfying chosen parameters:	76		
Minimum DB seq length:	14		
Maximum DB seq length:	14		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
Database :	SwissProt_42.2*		
Pred. No.	Score	Query Match Length DB ID	Description
1	22	31.0 TAT_HV1W2	P12509 human immun
2	22	31.0 TAT_HV1Z8	P12511 human immun
3	16	22.5 TAT_SELM1	P2533 selenastrum
4	15	21.1 SAP2_ARBU	P11760 arbacia pun
5	14.5	20.4 FS19_CLOPP	Q46228 clover pro1
6	14	20.4 FS59_HORSE	Q4897 loofah witz
7	14	19.7 FTBA_HORSE	P14452 equus cabal
8	14	19.7 FTBB_MANLE	P14474 mandrillus
9	13	18.3 CXA1_CONCH	P25897 conus conso
10	13	18.3 CXA1_CONNA	P01521 conus magus
11	13	18.3 NEU2_FASHE	P80526 fasciola he
12	13	18.3 PPK6_PERAM	P82693 periplaneta
13	13	18.3 UN46_CLOPA	P8136 clostridium
14	12	16.9 CAT2_FASHE	P80342 fasciola he
15	12	16.9 COCO_LIMPO	P35586 limulus pol
16	12	16.9 DC04_VAIZE	P80101 zea mays (m
17	12	16.9 UN37_CLOPA	P2158 clostridium
18	11	15.5 GPKP_STRGR	P25013 streptomyce
19	11	15.5 RS19_PRUAP	Q44160 prunus arme
20	11	15.5 SK3_BEIQU	P45661 leiurus qui
21	10	14.1 CX1A_CONBE	P58633 conus betui
22	10	14.1 GLGS_SPIOL	P55235 spinacia ol
23	10	14.1 GR75_CANFA	P9950 canis famili
24	10	14.1 JAP1_RANJA	P83305 rana japoni
25	10	14.1 KARA_BROPL	P22442 bromelia pl
26	10	14.1 MARI_ALTSP	P29399 alteromonas
27	10	14.1 MY14_PHEVI	P46940 phaeotima v
28	10	14.1 NEK2_SARBU	P41433 sarcophaga
29	10	14.1 PH1_BRUISE	P29233 prunus sero
30	10	14.1 RS19_PWM	Q52083 pigeon pea
31	10	14.1 SNS1_MYOSC	P2070 myoxocephal
32	10	14.1 SMS_ALMIC	P3185 alligator m
33	10	14.1 SDN9_STRGR	P08732 streptomyce

TAT_HV1B8 STANDARD; PRT; 14 AA.

ID P12511; Rel. 12, Created)

AC DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 01-OCT-1989 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

TAT Protein (transactivating regulatory protein) (Fragment).

DE

GN Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).

OS Viruses; Retroviridae; Lentiviruses.

OC Retrovirus; Retroviridae; Lentiviridae.

OX NCBI_TaxID=11681;

RN SEQUENCE FROM N.A.

RP MEDLINE=88281278; PubMed=3395517;

RX Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F., Gallo R.C.;

RA "Nucleotide sequence analysis of the env gene of a new Zairian isolate of HIV-1."

RT AIDS Res. Hum. Retroviruses 4:165-173 (1988).

RL AIDS Res. Hum. Retroviruses 4:165-173 (1988).

CC -!- FUNCTION: Transcriptional regulator that acts by binding to the trans-activating responsive sequence (TAR) RNA element and activates transcription initiation and/or elongation from the LTR promoter.

CC -!- SUBUNIT: Binds cyclin T1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.

CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD ZAIREAN MALE.

CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>).

CC DR EMBL; J03653; AAA4485.1; -.

CC DR HIV; J03653; TATJYI.

CC DR Transcription regulation; Activator; RNA-binding; Nuclear protein; AIDS.

CC KW AIDS.

FT NON_TER 1 1

SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match Score 22; DB 1; Length 14;

Best Local Similarity 31.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

FT NON_TER 1 1

SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match Score 22; DB 1; Length 14;

Best Local Similarity 31.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

CC -!- SUBUNIT: Heterodimer of a 40 kDa and a 41 kDa subunit.

CC -!- SIMILARITY: Belongs to the phosphoribulokinase family.

DR InterPro; IPR000082; PRK.

DR PROSITE; PS00567; PHOSPHORIBULOKINASE; PARTIAL.

KW Transerase; Kinase; Calvin cycle; ATP-binding.

FT NON_TER 14 14

SQ SEQUENCE 14 AA; 1379 MW; C4B1DBCD2F891062 CRC64;

Query Match Score 16; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

SAP2_ARBPU STANDARD; PRT; 14 AA.

ID SAP2_ARBPU

AC PL1760;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 01-OCT-1989 (Rel. 42, Last annotation update)

DR Resact (Sperm-activating Peptide) (SAP-IIA).

OS Arbacia punctulata (Punctuated sea urchin).

CC Eukaryota; Metazoa; Echinodermata; Echinerozoa; Echinidae; Echinoidea; Euechinoidea; Arbacidae; Arbacidae; Arbacidae.

NCBI_TaxID=7641;

OX RN

RP TISSUE=Egg;

RC MEDLINE=85054981; PubMed=6150045;

RA Suzuki N., Shimomura H., Radany E.W., Ramarao C.S., Ward G.E., Bentley J.K., Gerbers D.L;

RA "A peptide associated with eggs causes a mobility shift in a major plasma membrane protein of spermatozoa.";

RA J. Biol. Chem. 259:14874-14879 (1984).

RN DISULFIDE BOND.

RP MEDLINE=92097763; PubMed=1756858;

RA Yoshino K.-I., Takao T., Shimomishi Y., Suzuki N.;

RT "Determination of the amino acid sequence of an intramolecular disulfide linkage-containing sperm-activating peptide by tandem mass spectrometry";

RT FEBS Lett. 294:179-182 (1991).

CC -!- FUNCTION: Cause stimulation of sperm respiration and motility through intracellular alkalization, transient elevations of cAMP, cGMP and calcium levels in sperm cells, and transient activation and subsequent inactivation of the membrane form of guanylate cyclase.

CC -!- SIMILARITY: SMALL TO S_PURPURATUS SPERACT.

KW Amidation.

FT DISULFID 1 8

FT MOD_RES 14 14 AMIDATION

SQ SEQUENCE 14 AA; 1246 MW; 39745A933BBE41B8 CRC64;

Query Match Score 15; DB 1; Length 14;

Best Local Similarity 57.1%; Pred. No. 7.7e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

CC -!- CKGDSCG 11

CC 8 CVG-GG 12

OX NCBI_TaxID=39955;

RN SEQUENCE.

RA Lin M., Turpin D.H.;"Purification and molecular and immunological characterization of a unique phosphoribulokinase from the green alga *Selenastrum minutum*.";

RT Plant Physiol. 98:882-88 (1992).

CC -!- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-ribulose 1,5-bisphosphate.

CC -!- PATHWAY: Calvin Cycle.

OX NCBI_TaxID=39955;

RESULT 5

RS19_CLOPP STANDARD; PRT; 14 AA.

ID RS19_CLOPP

AC Q46228;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

OS *Fasciola hepatica* (Liver fluke).
 OC Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomatida; Fasciolidae; Fasciidae;
 OC Clostridiaceae;
 OX NCBI_TaxID=6192;
 RN [1]
 SEQUENCE
 MEDLINE=95366993; PubMed=7619732;
 RX RT "Fasciola hepatica: rapid identification of newly excysted juvenile
 proteins.";
 RL Biochim. Biophys. Res. Commun. 213:169-174(1995).
 CC -|- DEVELOPMENTAL STAGE: Expressed at the newly excysted juvenile
 stage.
 CC FT NON_TER 14
 SEQUENCE 14 AA; 1581 MW;
 SQ Query Match Similarity 18.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 8 DSG 10
 DB 3 DNG 5

RESULT 12
 PPKE_PERAM PERAM STANDARD; PRT; 14 AA.
 ID AC PB1693;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 OS Pyrokinin-6 (Pea-PK-6) (FXPLR-amide).
 Periplaneta americana (American cockroach)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Diptera; Orthopterida; Dictyoptera; Blattaria;
 OC Blattidae; Periplaneta; Blattaria; Blattoidea;
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomatida; Echinostomatida; Fasciidae; Fasciolidae.
 OX NCBI_TaxID=6972;
 RN [1]
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal parasympathetic organs, and Corpora cardiaca;
 RX MEDLINE=9403913; PubMed=8033913;
 RA Predeil R., Eckert M.;
 RT "Tissue-specific distribution of FXPLRlamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363 (2000).
 CC -|- FUNCTION: Shows a weakly myoactive action.
 CC -|- TISSUE SPECIFICITY: Corpora allata and to a lesser extent in
 abdominal parasympathetic organs.
 CC -|- MASS SPECTROMTRY: MW=1590.8; METHOD=WALDI.
 CC -|- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro; IPR01444; Pyrokinin.
 DR Amidation; Pyrokinin.
 MOD RES 14
 SEQUENCE 14 AA; 1592 MW;

Query Match Similarity 18.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GP 12
 DB 11 GP 12

RESULT 13
 UN46_CLOPA CLOPA STANDARD; PRT; 14 AA.
 ID UN46_CLOPA
 AC P81362;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Unknown protein CP 46 from 2D-page (Fragment).
 OS Clostridium Pasteurelum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP STRAIN=WS;
 RX MEDLINE=96291870; PubMed=9629918;
 RA Flengsrød R., Skjeldal L.;
 RL "Two-dimensional gel electrophoresis separation and N-terminal
 sequence analysis of proteins from Clostridium pasteurianum WS.";
 RL Electrophoresis 19:802-806 (1998).
 CC -|- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.4, ITS MW IS: 38.2 kDa.
 CC FT NON_TER 14
 SQ SEQUENCE 14 AA; 1550 MW; 198078P4C0367170 CRC64;
 Query Match Similarity 18.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 42.9%; Pred. No. 1.e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GDACXGD 8
 DB 8 GNNNIGD 14

RESULT 14
 CAT2_FASHE FASHE STANDARD; PRT; 14 AA.
 ID CAT2_FASHE
 AC P80372;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 41, Last annotation update)
 DT 28-PEB-2003 (Rel. 41, Last annotation update)
 DE Cathepsin L2 (BC 3.4.22.15) (Fragment).
 OS Fasciola hepatica (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomatida; Echinostomatida; Fasciidae; Fasciolidae.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94307282; PubMed=8033913;
 RA Dowd A.J., Smith A.M., McGonigle S., Dalton J.P.;
 RT "Purification and characterisation of a second cathepsin L protease
 secreted by the parasitic trematode *Fasciola hepatica*.";
 RL J. Biochem. 223:91-98 (1994).
 CC -|- FUNCTION: Thiol protease that assists the parasite in burrowing
 through the gut wall and liver of its mammalian host.
 CC -|- CATALYTIC ACTIVITY: Specificity close to that of papain. As
 compared to cathepsin B, cathepsin B exhibits higher activity
 towards protein substrates but has little activity on Z-Arg-Arg-
 NHMe, and no peptidyl-di-peptidase activity.
 CC -|- SUBUNIT: Dimer of a heavy and a light chain linked by disulfide
 bonds.
 CC -|- SUBCELLULAR LOCATION: Lysosomal.
 CC -|- SIMILARITY: Belongs to peptidase family C1.
 DR PIR: S45655; S45655.
 DR MEROPS: C01_033; -.
 DR InterPro: IPR00167; SHPrOc_scissite.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; PARTIAL.
 DR PROSITE: PS00039; THIOL_PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOL_Protease ASN; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1605 MW; 9CATAB749DA110A CRC64;

Query Match Similarity 16.9%; Score 12; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2.3e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 8 DSG 10
 DB 10 ESG 12

RESULT 15

COCO_LIMPO	STANDARD;	PRT;	14 AA.
ID COCO_LIMPO			
AC P35586;			
DT 01-JUN-1994	(Rel. 29, Created)		
DT 01-JUN-1994	(Rel. 29, Last sequence update)		
DT 28-FEB-2003	(Rel. 41, Last annotation update)		
DE Cocoanase (EC 3.4.21.-) (Fragment).			
OS Limulus polyphemus (Atlantic horseshoe crab).			
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;			
OC Limulidae; Limulus.			
OX NCBI_TaxID=6850;			
RN [1]			
RP SEQUENCE.			
RX MEDLINE=78037243; PubMed=335821;			
RA Law J.H., Dunn P.E., Kramer K.J.;			
RT "Insect proteases and peptidases.";			
RL Adv. Enzymol. Relat. Areas Mol. Biol. 45:389-425(1977).			
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.			
CC -!- SUBCELLULAR LOCATION: Extracellular.			
CC -!- SIMILARITY: Belongs to peptidase family S1.			
DR MEROPS: S01.112;			
DR InterPro: IPR001254; Peptidase_S1.			
DR PROSITE: PS00240; TRIPSIN_DOM; PARTIAL.			
DR PROSITE: PS00134; TRIPSIN_HIS; PARTIAL.			
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.			
KW Hydrolase; Serine protease.			
FT NON_TER 14 AA; 1452 MW; 1615FB1D73747570 CRR64;			
SQ SEQUENCE.			

Query Match Similarity 16.9%; Score 12; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GG 11			
Db 3 GG 4			

Search completed: February 26, 2004, 09:41:05
 Job time : 13 secs

GanCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:38:57 ; Search time 39 Seconds

(without alignments)
113.263 Million cell updates/sec

Title: US-09-909-348-4
 Perfect score: 71
 Sequence: 1 RGDACTGDSGPXV 14

Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 14
 Maximum DB seq length: 14

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_hexamer:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 14
 Maximum DB seq length: 14

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archea:*

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4: sp_hexamer:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

ALIGNMENTS

RESULT 1	ID	Q8BA40	PRELIMINARY;	PRT;	14 AA.
	AC	Q8B400;			
	DT	01-NOV-1996 (TREMBLrel. 01, Created)			
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
	DB	Tax Protein (Fragment).			
	GN				
	OS	Simian T-lymphotropic virus 1.			
	OC	Viruses; Retroviruses; Retroviridae; Deltaretrovirus.			
	OX	NCBI_TaxID=33747;			
	RN	[1]			
	RP	SEQUENCE FROM N_A.			
	RX	MEDLINE=9408462; PubMed=8259665;			
	RA	Saksena N.K., Herve V., Durand J.P., Leguenno B., Diop O.M.,			
	RA	Dicoutre J.P., Marthior C., Muller M.C., Love J.L., Benz P.M.,			
	RA	Brenot S., Barre-Sinoussi F., Poiesz B.J.;			
	RT	"Seroepidemiologic, molecular, and phylogenetic analyses of simian T-cell leukemia viruses (STLV-1) from various naturally infected monkey species from central and western Africa."			
	RL	Virology 198:297-310 (1993).			
	DR	EMBL: L20363; AAA7870; 1;			
	DR	GO: GO:0016553; P: transcriptional activator activity; IEA,			
	DR	GO: GO:0045941; P: positive regulation of transcription; IEA.			
	DR	InterPro: IP004120; Tax.			
	DR	Pfam: PF02959; Tax: 1;			
	FT	NON_TER 1 1			
	FT	SEQUENCE 14 AA; 1394 MN;			
	SQ	8BA772659C6D387A CRC64;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2.6	36.6	14	15 Q8B400	Q8B400 simian t-ly
2	2.2	31.0	14	15 Q8JDM3	Q8JDM3 human immun
3	2.2	31.0	14	15 Q8JDM7	Q8JDM7 human immun
4	2.2	31.0	14	15 Q8JDM0	Q8JDM0 human immun
5	2.1	29.6	14	10 Q8S939	Q8S939 beta vulgar
6	1.9	26.8	14	5 Q8B502	Q8B502 schistosoma
7	1.9	26.8	14	10 P82322	P82322 pisum sativ
8	1.9	26.8	14	10 Q7X9S0	Q7X9S0 malus domes
9	1.8	25.4	14	4 Q7Z7B2	Q7Z7B2 homo sapien
10	1.8	25.4	14	6 Q9TR83	Q9TR83 sus scrofa
11	1.7	23.9	14	3 Q8JIG5	Q8JIG5 ashyra gross
12	1.7	23.9	14	4 Q16045	Q16045 homo sapien
13	1.7	23.9	14	5 Q26675	Q26675 psammochilus
14	1.7	23.9	14	11 Q8CJA8	Q8CJA8 mus musculus
15	1.6	22.5	14	2 Q8VQ14	Q8VQ14 microccocus
16	1.6	22.5	14	4 Q8NIA6	Q8NIA6 homo sapien

Qy	2 GDA2XGBD---SGG 11
Db	1 GDCVQGDWCPISGG 14

Query Match Similarity 25.4%; Score 18; DB 6; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 DSGG 11
Db 3 DEGG 6

RESULT 13

```

QY 1 RGDAC 5
  | |
  4 RGPHC 8

DB 26075 PRELIMINARY;
  ID Q26075
  AC Q26075;
  DT 01-NOV-1996 (TRIMBLRE). 01, Created
  DT 01-DEC-2001 (TRIMBLRE). 01, Last sequence update
  DB Histone H2A (Fragment)
  OS Psammechinus miliaris (Sand sea urchin)
  OC Eukaryota; Metazoa; Echinodermata; Echinzoa;
  OC Echinoidea; Euechinoidea; Echinidae;
  OC Psammechinus
  OC NCBI_TaxID=1660;
  RN [1]
  RP SEQUENCE FROM N.A.
  RX MEDLINE=85104235; PubMed=2858095;
  RA Nordstrom J.L., Hall S.L., Kessler M.M./
  "Polyadenylation of sea urchin histone RNA sequences in transfected
  COS cells."
  RT PROC. Natl. Acad. Sci. U.S.A. 82:1094-1098 (1985).
  RL DR EMBL; M12542; AAA30028.1; -
  FT NON TER 1 1
  FT CHAIN 1 9 HISTONE H2A.
  SQ SEQUENCE 14 AA; 1620 MW;
  QY 9 SGGPXPV 14
  RP Score 17; DB 5; Length 14;
  Best Local Similarity 50.0%; Pred. No. 2.8e+04;
  Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
  DB 6 SGPPNT 11

```

RESULT 14

```

Q8CJA8 PRELIMINARY;
  ID Q8CJA8
  AC Q8CJA8;
  DT 01-MAR-2003 (TRIMBLRE). 23, Created
  DT 01-MAR-2003 (TRIMBLRE). 23, Last sequence update
  DB Methylelenetetrahydrofolate reductase short isoform (Fragment).
  GN MTTHFR.
  OS Mus musculus (Mouse)
  OC Buiaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
  OC NCBI_TaxID=10090;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN=129/Sv;
  RX MEDLINE=22257759; PubMed=12370778;
  RA Tran P., Leclerc D., Chan N., Pai A., Hiou-Tim F., Wu Q., Goyette P.,
  Artigas C., Milos R., Rozen R., -
  RA DR AP404271; AAN40873.1; -
  RT MGD; MGI:1066339; Mchfr.
  FT NON TER 14 14
  SQ SEQUENCE 14 AA; 1472 MW;
  QY 9 SGGPXPV 12
  RP Score 17; DB 11; Length 14;
  Best Local Similarity 75.0%; Pred. No. 2.8e+04;
  Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Query Match Similarity 23.9%; Score 17; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GBGGP 12
Db 3 GSCTGP 8

RESULT 12

```

Q16045 PRELIMINARY;
  ID Q16045
  AC Q16045;
  DT 01-NOV-1996 (TRIMBLRE). 01, Created
  DT 01-NOV-1996 (TRIMBLRE). 01, Last sequence update
  DB D3 dopamine receptor (Fragment).
  GN D3R.
  OS Homo sapiens (Human)
  OC Buiaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Mammalia; Eutheria; Primates; Primates; Catarrhini; Hominidae; Homo.
  OC Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Mammalia; Eutheria; Primates; Primates; Catarrhini; Hominidae; Homo.
  OC NCBI_TaxID=9606;
  RN [1]
  RP SEQUENCE FROM N.A.
  TISSUE-BLOOD;
  RX MEDLINE=93326145; PubMed=7916609;
  RA Negai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;
  RT "Expression of the D3 dopamine receptor gene and a novel variant
  transcript generated by alternative splicing in human peripheral blood
  lymphocytes";
  RT Biochem. Biophys. Res. Commun. 194:368-374 (1993).
  DR EMBL; S63845; AA2B254.2; -
  DR GO: GO:004812; F:receptor activity; IEA.
  KW Receptor.
  FT NON TER 1 1
  SQ SEQUENCE 14 AA; 1586 MW;
  QY 9 SGGPXPV 12
  RP Score 17; DB 5; Length 14;
  Best Local Similarity 50.0%; Pred. No. 2.8e+04;
  Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Query Match Similarity 23.9%; Score 17; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 SGGP 12

Db 8 SGSP 11

RESULT 15

QBVO14	PRELIMINARY;	PRT;	14 AA.
ID			
AC	QBVO14;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-TUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	ErmL leader peptide.		
OS	Micrococcus luteus (Micrococcus lysodictikticus).		
OG	Plasmid PMEC2.		
OC	Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;		
OC	Micrococccineae; Micrococcaceae; Micrococcus.		
OX	NCBI_TaxID=1270;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MW843;		
RA	Liebl, W.; Kloos, W.E.; Ludwig, W.;		
RT	"Plasmid-born macrolide-lincosamide-streptogramin B (MLS) resistance in Micrococcus luteus."		
RT	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AP062611; AAU68826; 1;		
GO	GO:0046822; C:extrachromosomal DNA; IEA.		
DR	Plasmid.		
KW	SEQUENCE 14 AA; 1625 MW;		
SQ	C6BF8E5F5CD58BCD CRC64;		

Query Match 22.5%; Score 16; DB 2; Length 14;
 Best Local Similarity 40.0%; Pred. No. 4.1e+04;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GGPXV 14
 Db 2 GSPSI 6

Search completed: February 26, 2004, 09:42:31
 Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:34:56 ; Search time 52 Seconds
(without alignments)

76.070 Million cell updates/sec

Title: US-09-909-348-4
Perfect score: 71
Sequence: 1 RGDACXGDSGPXV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282247505 residues

Total number of hits satisfying chosen parameters: 17938

Minimum DB seq length: 14
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database :

- 1: Geneseq_29Jan04:*
- 2: GeneseqP_1990s:*
- 3: GeneseqP_2000s:*
- 4: GeneseqP_2001s:*
- 5: GeneseqP_2002s:*
- 6: GeneseqP_2003aa:*
- 7: GeneseqP_2003gs:*
- 8: GeneseqP_2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	67	94.4	14 5 AAU78375	Aau78375 Thrombin
2	67	94.4	14 5 AAE20158	Aae20158 Human thr
3	67	94.4	14 5 ABB80264	Abb80264 Thrombin
4	53	74.6	14 5 AAE17240	Aae17240 Human tra
5	53	74.6	14 5 AAE18999	Aae18999 Human mat
6	48	67.6	14 5 AAB0522	Aab0522 Epithilin
7	38	53.5	14 4 AAG73193	Aag73193 Procase
8	32	45.1	14 3 AAY53773	Aay53773 Linker of
9	32	45.1	14 4 AAE08818	Aae08818 Synthetic
10	32	45.1	14 5 AAE29569	Aae29569 Metallope
11	32	45.1	14 5 AAE29631	Aae29631 Metallope
12	30	42.3	14 2 AAR93584	Aar93584 Dopamine
13	30	42.3	14 2 AAW10751	Aaw10751 Thrombin
14	30	42.3	14 4 ABP56804	Abp56804 Human SNP
15	30	42.3	14 4 ABP56805	Abp56805 Human SNP
16	29	40.8	14 2 AAR69303	Aar69303 GP IIb/III
17	29	40.8	14 2 AAM0586	Aam0586 GP IIb/III
18	29	40.8	14 2 ADD25483	Ad25483 Tc-99m la
19	29	40.8	14 3 AAY54969	Aay54969 Peptide I
20	29	40.8	14 3 AAY5454	Aay5454 GP IIb/III
21	29	40.8	14 4 AAC73186	Aac73186 Protease
22	29	40.8	14 4 AAC73194	Aac73194 Protease
23	27	38.0	14 2 AAM69149	Aam69149 Neuronal
24	27	38.0	14 4 AAM00734	Aam00734 Human pro-
25	27	38.0	14 5 ABP47204	Abp47204 Human BLY

ALIGNMENTS

26	26	36.6	14 2 AAR28561	Aar28561 Cell-to-cell
27	26	36.6	14 2 AAR28562	Aar28562 Cell-to-c
28	26	36.6	14 2 AAR28563	Aar28563 Cell-to-c
29	26	36.6	14 2 AAR28568	Aar28568 Human pep
30	26	36.6	14 4 AAM97046	Aam97046 Human str
31	26	36.6	14 4 AAM00571	Aam00571 Human str
32	26	36.6	14 5 ABG92752	Abg92752 B. brevis
33	25	35.2	14 2 AAY22932	Aay22932 Peptide d
34	25	35.2	14 3 AAY77498	Aay77498 Caspase a
35	25	35.2	14 4 AAM98037	Aam98037 Human pep
36	25	35.2	14 4 AAB47632	Aab47632 PAR4 Pept
37	25	35.2	14 4 AAM00572	Aam00572 Human sin
38	25	35.2	14 4 ABB56384	Abb56384 Integrin
39	25	35.2	14 4 AAB46396	Abp46396 Human BLY
40	25	35.2	14 5 ABP47207	Abp47207 Synthetic
41	25	35.2	14 6 ABG98507	Abg98507 Synthetic
42	25	35.2	14 7 ADD28974	Add28974 Staurospo
43	25	35.2	14 7 AAR88843	Aar88843 CDR switch
44	24	33.8	14 2 AAW22222	AAw22222 Spacer pe

RESULT 1

AXU78375	ID	AAU78375	standard; peptide; 14 AA.	
XX	AC	AAU78375;		
XX	DT	18-JUN-2002	(first entry)	
XX	DE	Thrombin peptide derivative #2.		
XX	XX	Thrombin; osteopathic; receptor; agonist; bone growth stimulation; osteoinduction; farm animal; companion animal; laboratory animal; bone graft; segmental bone gap; bone void; non-union fracture.		
OS	XX	Synthetic.		
XX	FT	Key	Location/Qualifiers	
XX	FT	Misc-difference	7 /label= Glu, Gln	
FT	FT	FT	13 /label= Phe, Met, Leu, His, Val	
XX	XX	XX	XX	WO200205836-A2.
XX	XX	XX	XX	24-JAN-2002.
XX	XX	XX	XX	18-JUL-2001; 2001WO-US022641.
PR	PR	PR	PR	19-JUL-2000; 2000US-0219300P.
XX	XX	XX	XX	(TEXA) UNIV TEXAS SYSTEM.
PA	PA	PA	PA	Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
XX	XX	XX	XX	WPI; 2002-303796/34.
PT	PT	PT	PT	Stimulating bone growth at a site in a subject in need of osteoinduction, such as a site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated thrombin receptor.
XX	XX	XX	XX	Claim 10; Page 22; 27PP; English.
CC	CC	CC	CC	The invention describes a method of stimulating bone growth at a site in a subject in need of osteoinduction. The method involves administering an agonist to stimulate bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoinduction, such as the site in need of a bone graft in a subject, a segmental bone gap, a bone void or a non-union fracture. This sequence

(EIDG-) EIDGENÖSSISCHE TECH HOCHSCHULE ZUERICH.
 XX Neri D, Tarli L, Viti F, Birchler M;
 XX WPI; 2000-039074/03.
 XX Fibronectin ED-B domain epitope specific antibodies and conjugate
 PT antibodies.
 XX Claim 10; Page 38; 59pp; English.
 XX The present sequence represents a linker component of a modified human
 CC scFv antibody which has specific affinity for a characteristic epitope of
 CC the ED-B domain of fibronectin. The affinity of the antibody for this
 CC epitope was improved by introducing a number of mutations in the
 CC complementarity determining region (CDR) residues located at the
 CC periphery of the binding site. The improved antibody is used for rapid
 CC targeting markers of angiogenesis, for detecting diseases characterized
 CC by vascular proliferation, such as diabetic retinopathy, age-related
 CC macular degeneration or tumours. The antibody localizes the respective
 CC immunosintigraphic detection of angiogenesis and for diagnosis and
 CC therapy of tumours and diseases characterized by vascular proliferation.
 CC The antibody can be conjugated to a molecule which induces blood
 CC coagulation and blood vessel occlusion. These conjugates are used in the
 CC preparation of injectable compositions for the treatment of angiogenesis-
 CC related pathologies, especially caused by or associated with ocular
 CC angiogenesis.
 XX Sequence 14 AA;

Query Match 9
 Best Local Similarity 45.1%; Score 32; DB 3; Length 14;
 ID AAE08818; Pred. No. 7.7e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0;
 Gaps 0;
 QY 2 GDACKEDSGG 11
 Db 1 GDSSGGSGG 10

RESULT 9
 AAE08818
 ID AAE08818 standard; protein; 14 AA.
 XX
 AC AAE08818;
 DT 19-NOV-2001 (first entry)
 XX Synthetic peptide linker for constructing ScFv L19 antibody.
 DE
 XX ScFv; single-chain variable antibody fragment; cancer; cytotoxic;
 KW coagulant; ED-B domain; fibronectin; tumor; ocular disorder; psoriasis;
 KW vascular proliferation; rheumatoid arthritis; blood vessel occlusion;
 KW angiogenesis; blood coagulation.
 XX
 OS Synthetic.
 PN WO200162800-A1.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-EP002062.
 XX
 PR 24-FEB-2000; 2000US-00514082.

XX (EIDG-) EIDGENÖSSISCHE TECH HOCHSCHULE ZUERICH.
 PA Neri D, Tarli L, Viti F, Birchler M;
 XX WPI; 2001-541701/60.
 XX An antibody, with specific affinity for a characteristic epitope of the
 PT ED-B domain of fibronectin for the treatment of diseases characterized by

PT vascular proliferation.
 XX Claim 10; Page 36; 73pp; English.
 XX
 CC The invention relates to an antibody with specific affinity for a characteristic epitope of the BD-B domain of fibronectin, where the antibody has improved affinity to BD-B. The invention also relates to conjugates comprising antibodies with a suitable photoactive molecule useful in the detection and/or coagulation of blood vessels. An antibody with improved affinity to the BD-B domain is useful for diagnosis and CC therapy of tumors and diseases characterised by vascular proliferation, cancer, rheumatoid arthritis, neo-vasculature associated ocular disorders CC and psoriasis. Treatment of angiogenesis related pathologies comprises CC the injection of conjugates comprising antibody and a molecule capable of CC inducing blood coagulation and blood vessel occlusion. The present CC sequence is a peptide linker used for constructing single-chain variable CC antibody fragment (scFv) L19 antibody related to the invention
 CC XX Sequence 14 AA;
 Query Match 10
 Best Local Similarity 45.1%; Score 32; DB 4; Length 14;
 ID AAE29569 standard; peptide; 14 AA.
 XX
 AC AAE29569;
 XX DT 27-JAN-2003 (first entry)
 DE Metallopeptide #13 used for Prion disease treatment.
 XX
 KW Metallopeptide; nortropic; amyloid beta-protein; Alzheimer's disease; AD;
 KW Prion's disease; neuroprotective; neuroprotection;
 KW therapy.
 OS Unidentified.
 XX Key
 FT Msc-difference 3 /label= Pro, Gly, Ala
 XX
 PN WO200264734-A2.
 XX 22-AUG-2002.
 PR 19-DEC-2001; 2001WO-US050075.
 XX
 PR 19-DEC-2000; 2000US-0256842P.
 PR 11-JUL-2001; 2001US-034835P.
 PR 04-OCT-2001; 2001US-0327835P.
 XX
 PA (PALA-) PALATIN TECHNOLOGIES INC.
 XX
 PI Sharma SD, Shi Y;
 XX DR WPI; 2002-740699/80.
 XX Determining secondary structure binding to desired targets within parent
 PT polypeptides that bind to target, by constructing and complexing
 PT peptides to metal ions to form metallopeptides.
 PT XX PS Example 3; Page 140; 165pp; English.
 CC The invention relates to a method for identification and determination of

target-specific folding sites in peptides and proteins. The invention also relates to a method for determining a secondary structure binding to desired targets within parent polypeptides that bind to targets, by constructing and complexing peptides to metal ions to form metallopeptides and screening the metallopeptides. The method is useful for determining secondary structure binding to desired target within parent polypeptides and screening the metallopeptides. The method is useful for determining secondary structure binding to desired target within parent polypeptide with primary structure that binds to the target, where the target of interest is a receptor, antibody, toxin, enzyme, hormone, nucleic acid, intracellular protein domain of biological relevance or extracellular protein domain of biological relevance. A library of amyloid beta-protein related peptides is useful for the treatment of Alzheimer's disease (AD). A library of peptides targeting vasopressin, oxytocin or angiotensin receptor is useful for treating Prion's disease. The present sequence is metallopeptide used for Prion disease treatment. This peptide is used to illustrate the method of the invention

XX Sequence 14 AA;
 XX Query Match. Score 32; DB 5; Length 14;
 XX Best Local Similarity 58.3%; Pred. No. 7.7e+02;
 XX Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX Qy 3 DACKGDGGXV 14
 XX Db 1 DACKAPAPGAV 12

RESULT 11
 AAE29631 standard; peptide: 14 AA.
 XX ID AAE29631 standard; peptide: 14 AA.
 XX AC AAE29631;
 XX DT 27-JAN-2003 (first entry)
 XX DE Metallopeptide #16 used for Prion disease treatment.
 XX KW Metallopeptide; nootropic; amyloid beta-protein; Alzheimer's disease; neuroprotective; AD; Prion's disease; oxytocin; vasopressin; neuroprotective; AD; KW therapy.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Misc-difference 4 /label= Pro, Gly, Ala
 XX PN WO200264734-A2.
 XX PD 22-AUG-2002.
 XX PP 19-DEC-2001; 2001WO-US050075.
 XX PR 19-DEC-2000; 2000US-0256842P.
 XX PR 11-JUL-2001; 2001US-0304835P.
 XX PR 04-OCT-2001; 2001US-0327835P.
 XX (PALA-) PALATIN TECHNOLOGIES INC.
 XX Sharma SD, Shi Y;
 XX WPI; 2002-740699/30.

XX DR 2002-740699/30.
 XX PT Determining secondary structure binding to desired targets within parent polypeptides that bind to targets, by constructing and complexing the metallopeptides.
 XX PT Example 3; Page 157; 165pp; English.
 XX PS The invention relates to a method for identification and determination of target-specific folding sites in peptides and proteins. The invention also relates to a method for determining a secondary structure binding to

CC desired targets within parent polypeptides that bind to targets, by constructing and complexing peptides to metal ions to form metallopeptides and screening the metallopeptides. The method is useful for determining secondary structure binding to desired target within parent polypeptides and screening the metallopeptides. The method is useful for determining secondary structure binding to desired target within parent polypeptide with primary structure that binds to the target, where the target of interest is a receptor, antibody, toxin, enzyme, hormone, nucleic acid, intracellular protein domain of biological relevance or extracellular protein domain of biological relevance. A library of amyloid beta-protein related peptides is useful for the treatment of Alzheimer's disease (AD). A library of peptides targeting vasopressin, oxytocin or angiotensin receptor is useful for treating Prion's disease. The present sequence is metallopeptide used for Prion disease treatment. This peptide used to illustrate the method of the invention

XX SQ Sequence 14 AA;
 XX Query Match. Score 32; DB 5; Length 14;
 XX Best Local Similarity 58.3%; Pred. No. 7.7e+02;
 XX Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX Qy 3 DACKGDGGXV 14
 XX Db 1 DACKAPAPGAV 12

RESULT 12
 AAR93584 standard; peptide: 14 AA.
 XX ID AAR93584

XX AC AAR93584;
 XX DT 08-OCT-1996 (first entry)
 XX DB Dopamine receptor isoform D5 Peptide analogue (aa: 23-35-Cys36).
 XX KW Dopamine; identification; neurotransmitter; diagnosis; analogue; isoform-specific antibody; receptor; distinction; identification; Parkinson's disease; Alzheimer's disease; neurological.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "opt. acetylated"
 XX PN WO9606856-A1.
 XX PD 07-MAR-1996.
 XX PF 30-AUG-1995;
 XX PR 31-ARG-1994;
 XX PA (WEBB/) WEBBER R.
 XX PI Webber R;
 XX DR WPI; 1996-160304/16.

XX PT Peptide analogues of different dopamine receptor isoform(s) - also antibodies raised against them, useful in drug development and diagnosis, e.g. of Parkinson's disease.

XX PS Claim 1; Fig 5c; 56pp; English.
 CC AAR93582-R93586 are peptide analogues of the dopamine receptor isoform D5. The analogues correspond to regions that are variable between the five different isoforms, D1, D2, D3, D4 and D5 as such are specific for the particular isoform. The peptides or antibodies raised against them are useful in developing drugs for the treatment of and diagnosis of disorders related to the dopamine receptor e.g. Parkinson's disease and Alzheimer's disease

XX

SQ Sequence 14 AA;
 Query Match 42.3%; Score 30; DB 2; Length 14;
 Best Local Similarity 41.7%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Db 10 RGDAC 14

RESULT 14
 ABB56804 standard; peptide; 14 AA.
 ID ABB56804
 XX
 AC ABB56804;
 XX
 DT 05-MAR-2002 (first entry)
 XX Human SNP related amino acid sequence SEQ ID NO:1369.
 DE Human SNP; polymorphism; SNP; cytostatic;
 XX single nucleotide Polymorphism; SNP; cytostatic;
 KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
 KW autoimmune disease; inflammation; cancer; nervous system disease;
 KW infection; polymorphic protein.

RESULT 13
 AAW10751
 ID AAW10751 standard; peptide; 14 AA.
 XX
 AC AAW10751;
 XX
 DT 29-AUG-1997 (first entry)
 DE Thrombin B chain active fragment #2.
 XX Thrombin; B-chain; active fragment; inhibitor; tumour metastasis; cancer;
 KW angiogenesis; melanoma; diabetic retinopathy; rheumatoid arthritis;
 KW RGD domain; therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO9700077-A1.
 XX
 PD 03-JAN-1997.
 XX
 PF 12-JUN-1995; 96WO-IL0000012.
 XX
 PR 14-JUN-1995; 95IL-00114140.
 XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PI Barshavit R;
 DR 1997-077354/07.
 XX Compson, for inhibiting tumour metastasis or angiogenesis - contains
 PT thrombin fragment contg. exposed RGD sequence, also related antibodies
 PT and method for assessing metastatic potential.
 XX
 PS Claim 2; Page 28; 45pp; English.
 XX AAW10750 and AAW10751 represent physiologically active fragments of the
 CC thrombin B-chain. This sequence corresponds to residues 17-191 of the
 CC native thrombin B-chain sequence. These sequences can be used in the
 CC composition of the invention for inhibiting tumour metastasis or
 CC angiogenesis, and for treating cancer. The composition comprises an
 CC active fragment of the thrombin B-chain (such as this sequence)
 CC containing the RGD sequence in an exposed orientation, an active modified
 CC thrombin with residues 187-189 (RGD), in exposed orientation, or an
 CC analogue of one of these. These RGD-containing fragments of thrombin are
 CC about 20 times more active as metastasis inhibitors than similar
 CC fragments from other proteins such as fibronectin. The composition is
 CC especially used for treating cancer or for determining the metastatic
 CC tendency of a tumour, especially melanoma allowing the most appropriate
 CC treatment to be selected. Other preferred applications of the anti-
 CC angiogenesis treatment are in diabetic retinopathy and rheumatoid
 CC arthritis. Antibodies which bind to the thrombin RGD domain can be used
 CC for screening active agents, i.e. selection of only those where RGD is
 CC exposed
 XX Sequence 14 AA;
 Query Match 42.3%; Score 30; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 SQ 1 RGDAC 5

RESULT 15
 ABB56805 standard; peptide; 14 AA.
 ID ABB56805
 Db 1 CQGDSG 6

Query Match 42.3%; Score 30; DB 4; Length 14;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CXGDSG 10
 Sq 1 CQGDSG 6

XX ABB56805;
 XX AC
 XX DT 05-MAR-2002 (first entry)
 XX DB Human SNP related amino acid sequence SEQ ID NO:1370.
 XX KW Human; single nucleotide polymorphism; SNP; Polymorphism; cytostatic;
 XX immuno suppressive; antiinflammatory; neuroprotective; antimicrobial;
 XX autoimmune disease; inflammation; cancer; nervous system disease;
 XX infection; polymorphic protein.

OS Homo sapiens.

XX WO200138586-A2.

XX PN 31-MAY-2001.

XX PD 22-NOV-2000; 2000WO-US032311.

XX PR 24-NOV-1999; 99US-0167383P.

XX (CURA-) CURAGEN CORP.

XX PA

XX PI Shimkets RA, Leach M;

XX DR 2001-355949/37.

XX PT Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism.

XX PS Claim 1; Page 650; 674pp; English.

CC ABL0010 to ABL01104 represent human nucleic acid oligonucleotides comprising one or more single nucleotide polymorphisms (SNPs). ABB56331 to ABB56903 represent human peptides encoded by some of the SNP oligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism. The pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterized polymorphism are present in individuals. The antibodies may be used in the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples).

XX Sequence 14 AA;

Query Match 42.3%; Score 30; DB 4; Length 14;
 Best Local Similarity 83.3%; Prd. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CXGDSG 10
 Db 1 CQGDSG 6

Search completed: February 26, 2004, 09:40:43
 Job time : 55 secs

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OM protein - protein search, using sw model.

Run on: February 26, 2004 09:41:42 ; Search time 33 Seconds
(without alignments)
89.580 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71 RGDAKGDGGPKV 14

Sequence: Sequence 16, App1

Scoring table: BLOSUM62 Sequence 10, App1

Gapop 10.0 , Gapext 0.5 Sequence 170, App

Searched: Sequence 173, App

809742 seqs, 21115259 residues Sequence 92, App1

Total number of hits satisfying chosen parameters: 6887 Sequence 195, App1

Minimum DB seq length: 14 Sequence 23, App1

Maximum DB seq length: 14 Sequence 23, App1

Post-processing: Minimum Match 0% Sequence 23, App1

Maximum Match 100% Sequence 23, App1

Listing First 45 summaries Sequence 23, App1

Database : Published Applications AA:^{*} Sequence 23, App11: /cgn2_6/prodata/2/pubpa/us07_PUBCOMB_pep:^{*} Sequence 23, App12: /cgn2_6/prodata/2/pubpa/us07_PCT_NEW_PUB_pep:^{*} Sequence 23, App13: /cgn2_6/prodata/2/pubpa/us05_NEW_PUB_pep:^{*} Sequence 23, App14: /cgn2_6/prodata/2/pubpa/us06_PUBCOMB_pep:^{*} Sequence 23, App15: /cgn2_6/prodata/2/pubpa/us07_NEW_PUB_pep:^{*} Sequence 23, App16: /cgn2_6/prodata/2/pubpa/PICTUS_PUCOMB_Pep:^{*} Sequence 23, App17: /cgn2_6/prodata/2/pubpa/us08_NEW_PUB_pep:^{*} Sequence 23, App18: /cgn2_6/prodata/2/pubpa/us09_PUCOMB_Pep:^{*} Sequence 23, App19: /cgn2_6/prodata/2/pubpa/us09_PUCOMB_Pep:^{*} Sequence 23, App110: /cgn2_6/prodata/2/pubpa/us09B_PUCOMB_Pep:^{*} Sequence 23, App111: /cgn2_6/prodata/2/pubpa/us09C_PUCOMB_Pep:^{*} Sequence 23, App112: /cgn2_6/prodata/2/pubpa/us09_NEW_PUB_pep:^{*} Sequence 23, App113: /cgn2_6/prodata/2/pubpa/us09_PUCOMB_Pep:^{*} Sequence 23, App114: /cgn2_6/prodata/2/pubpa/us10_PUCOMB_Pep:^{*} Sequence 23, App115: /cgn2_6/prodata/2/pubpa/us10C_PUCOMB_Pep:^{*} Sequence 23, App116: /cgn2_6/prodata/2/pubpa/us60_NEW_PUB_pep:^{*} Sequence 23, App117: /cgn2_6/prodata/2/pubpa/us60_NEW_PUB_pep:^{*} Sequence 23, App118: /cgn2_6/prodata/2/pubpa/us60_PUCOMB_Pep:^{*} Sequence 23, App1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	67	94.4	14	9 US-09-909-1122-4	Sequence 4, Appli
2	67	94.4	14	13 US-10-050-692-4	Sequence 4, Appli
3	67	94.4	14	13 US-10-050-688-4	Sequence 4, Appli
4	52	73.2	14	9 US-09-885-411-6	Sequence 6, Appli
5	32	45.1	14	10 US-09-300-425B-0	Sequence 20, Appli
6	32	45.1	14	14 US-10-321-558-31	Sequence 31, Appli
7	30	42.3	14	15 US-10-341-979-8	Sequence 8, Appli
8	27	38.0	14	10 US-09-880-148-315	Sequence 109, Appli
9	25	35.2	14	9 US-09-815-337-109	Sequence 3215, Appli
10	25	35.2	14	10 US-09-852-455-34	Sequence 34, Appli
11	25	35.2	14	10 US-09-852-455-35	Sequence 35, Appli
12	25	35.2	14	10 US-09-852-455-36	Sequence 36, Appli
13	25	35.2	14	10 US-09-852-455-37	Sequence 37, Appli
14	25	35.2	14	10 US-09-852-455-38	Sequence 38, Appli
15	25	35.2	14	10 US-09-880-748-3218	Sequence 3218, Appli

ALIGNMENTS

RESULT 1 US-09-909-1122-4

; Sequence 4, Application US/099091122

; Patent No. US20020128202A1

; GENERAL INFORMATION:

; APPLICANT: Carney, Darrell H.

; APPLICANT: Crowthier, Roger S.

; APPLICANT: Simmons, David J.

; APPLICANT: Yang, Jinping

; APPLICANT: Redin, William R.

; TITLE OF INVENTION: Peptide Growth With Thrombin

; FILE REFERENCE: 3033.1002-001

; CURRENT APPLICATION NUMBER: US/09/909,1122

; PRIORITY APPLICATION NUMBER: US 60/219,300

; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 4

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Peptide Fragment of Thrombin

; OTHER INFORMATION: Xaa at position six is Glu or Gln.

; NAME/KEY: VARIANT

; LOCATION: (1)-(14)

; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or Val

; OTHER INFORMATION: Xaa at position thirteen is Glu or Gln.

US-09-909-1122-4

Query Match Similarity 94.4%; Score 100.0%; Pred. No. 0.00066; Best Local Similarity 100.0%; Matches 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDAKGDGGPKV 14

Db 1 RGDAKGDGGPKV 14

RESULT 2
US-10-050-692-4
Sequence 4, Application US/10050692
Publication No. US20020182205A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES
FILE REFERENCE: 3,033,1002,004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 09/905,122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fragment of human prothrombin
FEATURE:
NAME/KEY: VARIANT
LOCATION: (6) .. (6)
OTHER INFORMATION: Xaa = Glu or Gln
FEATURE:
NAME/KEY: VARIANT
LOCATION: (13) .. (13)
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-4
Query Match 94.4%; Score 67; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGDA(XGDGSPXV 14
Db 1 RGDA(XGDGSPXV 14

RESULT 3
US-10-050-698-4
Sequence 4, Application US/10050688
Publication No. US20020198154A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Stieremberg, Janet
APPLICANT: Bergman, John
TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
FILE REFERENCE: 3,033,1003,004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence

RESULT 4
US-09-885-441-6
Sequence 6, Application US/09885441
Patent No. US2002146407A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human Eosinophil Serine
FEATURE:
FILE REFERENCE: 04974,00512
CURRENT APPLICATION NUMBER: US/09/885,441
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/212,844
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/244,171
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: US 60/279,766
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: BLOCKS domain

RESULT 5
US-09-885-441-6
Query Match 73.3%; Score 52; DB 9; Length 14;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 DACKGDSGGPXY 14
Db 2 DTCKGDBGGPLY 13

RESULT 5
US-09-300-425B-20
Sequence 20, Application US/09300425B
Publication No. US20030045881A1
GENERAL INFORMATION:
APPLICANT: Neri, Dario
APPLICANT: Tarli, Lorenzo
APPLICANT: Vitelli, Francesca
APPLICANT: Birtcher, Manted
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B

CURRENT FILING DATE: 1999-04-28
 PRIORITY APPLICATION NUMBER: 09/075, 338
 PRIOR FILING DATE: 1998-05-11
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 20
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: antibody linker
 OTHER INFORMATION: Description of Artificial Sequence: antibody linker
 US-09-300-425B-20

Query Match 45.1%; Score 32; DB 10; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GDACKGDSGG 11
 Db 1 GDSSGGGG 10

RESULT 8
 US-09-880-748-3215 ; Sequence 3215, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; APPLICANT: VITI, FRANCESCA
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; SEQ ID NO 3215
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-3215

Query Match 42.3%; Score 30; DB 15; Length 14;
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GDACKGDSGG 11
 Db 5 GDEVGGSOG 14

RESULT 6
 US-09-321-558-31 ; Sequence 31, Application US/10321558
 ; Publication No. US20030176663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NERI, DARIO
 ; APPLICANT: TARLI, LORENZO
 ; APPLICANT: VITI, FRANCESCA
 ; APPLICANT: BIRCHLER, MANFRED
 ; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
 ; FILE REFERENCE: NOTAR-1 C1
 ; CURRENT APPLICATION NUMBER: US/10/321,558
 ; CURRENT FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: 09/512,082
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 09/300,425
 ; PRIOR FILING DATE: 1999-04-28
 ; PRIOR APPLICATION NUMBER: 09/075,338
 ; PRIOR FILING DATE: 1998-05-11
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Linker sequence
 US-09-321-558-31

Query Match 45.1%; Score 32; DB 14; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GDACKGDSGG 11
 Db 1 GDSSGGGG 10

RESULT 9
 US-09-815-837-109 ; Sequence 109, Application US/09815837
 ; Publication No. US2003008411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hong Kong University of Science & Technology
 ; APPLICANT: Chang, Donald Choy
 ; APPLICANT: Luo, Qian Kathy
 ; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
 ; FILE REFERENCE: 3214183-1
 ; CURRENT APPLICATION NUMBER: US/10/341,979
 ; CURRENT FILING DATE: 2003-01-11

RESULT 7
 US-10-141-979-8 ; Sequence 8, Application US/10341979
 ; Publication No. US20040002128A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hong Kong University of Science & Technology
 ; APPLICANT: Chang, Donald Choy
 ; APPLICANT: Luo, Qian Kathy
 ; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
 ; FILE REFERENCE: 3214183-1
 ; CURRENT APPLICATION NUMBER: US/10/341,979
 ; CURRENT FILING DATE: 2003-01-11

RESULT 10
 US-09-815-837-109 ; Sequence 109, Application US/09815837
 ; Publication No. US2003008411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Immune Mediators and Related Methods
 ; FILE REFERENCE: 014058-00567005
 ; CURRENT APPLICATION NUMBER: US/09/815,837
 ; CURRENT FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: US 60/191,274
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: US 60/204,249
 ; PRIOR FILING DATE: 2000-05-15
 ; PRIOR APPLICATION NUMBER: US 60/264,003

PRIOR FILING DATE: 2001-01-23
 NUMBER OF SEQ ID NOS: 129
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 109
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:downstream
 OTHER INFORMATION: Linker for C0580 and C0587
 US-09-815-837-109

Query Match 35.2%; Score 25; DB 9; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GDSGGP 12
 Db 7 GSGGGP 12

RESULT 10
 US-09-852-455-34
 Sequence 34; Application US/09852455
 Publication No. US20030054348A1
 GENERAL INFORMATION:
 APPLICANT: BLUME, ARTHUR J.
 APPLICANT: GOLDSTEIN, NEIL
 APPLICANT: PILLUTA, RENIKA
 APPLICANT: HSIAO, KU-CHUAN
 APPLICANT: PREndergast, JOHN
 TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
 FILE REFERENCE: 2598-4004US1
 CURRENT APPLICATION NUMBER: US/09/852,455
 CURRENT FILING DATE: 2001-05-09
 PRIOR APPLICATION NUMBER: 60/202,912
 SEQ ID NO: 36
 LENGTH: 14

Query Match 35.2%; Score 25; DB 10; Length 14;
 Best Local Similarity 67.3%; Pred. No. 1.8e+03; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GDSGGP 12
 Db 7 GELGGP 6

RESULT 11
 US-09-852-455-35
 Sequence 35; Application US/09852455
 Publication No. US20030054348A1
 GENERAL INFORMATION:
 APPLICANT: BLUME, ARTHUR J.
 APPLICANT: GOLDSTEIN, NEIL
 APPLICANT: PILLUTA, RENIKA
 APPLICANT: HSIAO, KU-CHUAN
 APPLICANT: PREndergast, JOHN
 TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
 FILE REFERENCE: 2598-4004US1
 CURRENT APPLICATION NUMBER: US/09/852,455
 CURRENT FILING DATE: 2001-05-09
 PRIOR APPLICATION NUMBER: 60/202,912
 SEQ ID NO: 37
 LENGTH: 14

Query Match 35.2%; Score 25; DB 10; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;

Search completed: February 26, 2004, 09:47:14
Job time : 34 secs

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Db          2 RPDADYDGY 11
Db          2 RPDADYDGY 11

RESULT 14
US-09-852-455-38
; Sequence 38, Application US/09852455
; Publication No. US2003005348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENTUA
; APPLICANT: HSIAO, KU-CHIEN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-40041S1
; CURRENT APPLICATION NUMBER: US/09/52,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO: 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Felis catus
US -09-852-455-38

Query Match      Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      7 GDSGGP 12
Db      1 GEIIGGP 6

RESULT 15
US-09-880-3218
; Sequence 3218, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/980,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3218
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US -09-880-3218

Query Match      Score 25; DB 10; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.8e+03; Indels 4; Gaps 0;
Matches 6; Conservative 0; Mismatches 4; Indels 4; Gaps 0;
Qy      7 GDAACXGDG 10

```

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:39:42 ; Search time 23 Seconds
 (Without alignments)
 31.425 Million cell updates/sec

Title: US-09-909-348-4

Perfct score: 71

Sequence: 1 RGDAKXGDSGPXV 14

Scoring table: BLOSUM62

Scoring table: GappP 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 8296

Minimum DB seq length: 14

Maximum DB seq length: 14

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA!*

1: /cgns_6/podata/2/iaa/5A-COMB.pep *
 2: /cgns_6/podata/2/iaa/5B-COMB.pep *
 3: /cgns_6/podata/2/iaa/6A-COMB.pep *
 4: /cgns_6/podata/2/iaa/6B-COMB.pep *
 5: /cgns_6/podata/2/iaa/PECTUS-COMB.pep *
 6: /cgns_6/podata/2/iaa/backfile1.dep *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	6.7	94.4	14	4	US-09-631-137C-7	Sequence 7, Appli
2	3.0	42.3	14	3	US-08-981-088-4	Sequence 4, Appli
3	3.0	42.3	14	5	PCM-US91-11127-28	Sequence 28, Appli
4	2.9	40.8	14	2	US-08-935-832-10	Sequence 10, Appli
5	2.9	40.8	14	3	US-09-141-127-4	Sequence 4, Appli
6	2.6	36.6	14	1	US-07-994-162A-19	Sequence 19, Appli
7	2.6	36.6	14	5	PCM-US91-08228-35	Sequence 35, Appli
8	2.6	36.6	14	5	PCM-US91-08328-36	Sequence 36, Appli
9	2.6	36.6	14	5	PCM-US91-08228-37	Sequence 37, Appli
10	2.6	36.6	14	5	PCM-US91-08328-38	Sequence 38, Appli
11	2.5	35.2	14	3	US-0-441-507-43	Sequence 43, Appli
12	2.5	35.2	14	4	US-08-441-507-49	Sequence 49, Appli
13	2.5	35.2	14	4	US-07-969-872A-43	Sequence 43, Appli
14	2.4	33.8	14	2	US-08-487-431-2	Sequence 2, Appli
15	2.4	33.8	14	3	US-08-973-629-2	Sequence 2, Appli
16	2.4	33.8	14	3	US-09-091-814-8	Sequence 8, Appli
17	2.3	32.4	14	1	US-08-172-331B-10	Sequence 10, Appli
18	2.3	32.4	14	1	US-08-430-633-5	Sequence 5, Appli
19	2.3	32.4	14	1	US-08-471-780C-45	Sequence 45, Appli
20	2.3	32.4	14	1	US-08-471-780C-46	Sequence 46, Appli
21	2.3	32.4	14	1	US-0-467-288B-45	Sequence 45, Appli
22	2.3	32.4	14	1	US-08-467-288B-46	Sequence 46, Appli
23	2.3	32.4	14	2	US-08-448-418-101	Sequence 101, Appli
24	2.3	32.4	14	2	US-08-471-282A-45	Sequence 45, Appli
25	2.3	32.4	14	2	US-08-471-282A-46	Sequence 46, Appli
26	2.3	32.4	14	2	US-08-620-69A-5	Sequence 5, Appli
27	2.3	32.4	14	2	US-08-466-710C-45	Sequence 45, Appli

ALIGNMENTS

RESULT 1
 US-09-631-137C-7
 ; Sequence 7, Application US/09631137C
 ; PCT/US91-088-4
 ; GENERAL INFORMATION:
 ; APPLICANT: Carney, Darrell H.
 ; TITLE OF INVENTION: Thrombin Derived Polypeptides:
 ; FILE REFERENCE: Compositions and Methods for Use
 ; CURRENT APPLICATION NUMBER: US/09/631-137C
 ; CURRENT FILING DATE: 2000-08-07
 ; PRIOR APPLICATION NUMBER: US 08-538,504
 ; PRIOR FILING DATE: 1995-09-29
 ; PRIOR APPLICATION NUMBER: US 08/007,173
 ; PRIOR FILING DATE: 1993-01-21
 ; PRIOR APPLICATION NUMBER: US 06/925,201
 ; PRIOR FILING DATE: 1986-10-31
 ; SEQ ID NO: 7
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fragment of human prothrombin
 US-09-631-137C-7

Query Match 94.4%; Score 67; DB 4; Length 14;
 Best Local Similarity 85.7%; Prod. No. 0.00062;
 Matches 12; Conservative 0; Mismatches 2; Indexes 0; Gaps 0;

Qy 1 RGDACXGDSGPXV 14
 Db 1 RGDAECDGGPPFV 14

RESULT 2
 US-08-981-088-4
 ; Sequence 4, Application US/08981088
 ; PCT/US91-088-4
 ; GENERAL INFORMATION:
 ; APPLICANT: BAR-SHavit, RACHEL
 ; TITLE OF INVENTION: ANTI-METASTATIC AND ANTI-ANGIOGENIC
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OLIVE & BERRIDGE, PLC
 ; STREET: P. O. BOX 19328
 ; CITY: ALEXANDRIA

STATE: VA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01/981,088
FILING DATE: 27-JAN-1998
CLASSIFICATION: 514
NAME: OLIFF, JAMES A.
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 40455
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) - 836-6400
TELEFAX: (703) - 836-2787
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-981-088-4

Query Match 42.3%; Score 30; DB 3; Length 14;
Best Local Similarity 100.0%; Prod. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDAC 5
Db 10 RGDAC 14

RESULT 3
PCT-US95-11127-28
GENERAL INFORMATION:
APPLICANT: ROBERT WEBBER
TITLE OF INVENTION: DOPAMINE RECEPTOR PEPTIDES AND
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIELEN, PETERSON & LAMPE
STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720
CITY: WALNUT CREEK
STATE: CALIFORNIA
ZIP: 94596

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 5.25 INCH, 1.2 MB FOR FORMATTED
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11127
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NONE
FILING DATE: NONE
ATTORNEY/AGENT INFORMATION:
NAME: THEODORE J. BIELEN, JR.
REGISTRATION NUMBER: 27,420
REFERENCE/DOCKET NUMBER: 12068
TELEPHONE: (510) 937-1515
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
FEATURE:
NAME/KEY: DS RECEPTOR (AC-23-35Cys36)
LOCATION:
IDENTIFICATION METHOD: AMINO ACID ANALYSIS
OTHER INFORMATION: DOPAMINE DS RECEPTOR PEPTIDE
PCT-US95-11127-28

Query Match 42.3%; Score 30; DB 5; Length 14;
Best Local Similarity 41.7%; Prod. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGDACXGDSGP 12
Db 1 QGNAVGGSAGAP 12

RESULT 4
US-08-335-932-10
Sequence 10, Application US/08335832
Patent No. 5925311
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Thrombus Imaging
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,832
FILING DATE: 05-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5925311n, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,216-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-517
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Acm
/note= "This cysteine residue is blocked at the
sidechain sulfur by covalent linkage to an
acetamido group"
OTHER INFORMATION:
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /label= Acm
/note= "This cysteine residue is blocked at the

OTHER INFORMATION: sidechain sulfur by covalent linkage to an acetamido group"

US-08-335-822-10

Query Match Score 29; DB 2; Length 14;
Best Local Similarity 66.7%; Prod. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RGDAAXGDS 9
Db 6 RGDGGRGDS 14

RESULT 5
US-09-141-127-4

Sequence 4, Application US/09141127A

Patent No. 6083481

GENERAL INFORMATION:

APPLICANT: Dean, Richard T.

APPLICANT: Lister-James, John

TITLE OF INVENTION: THROMBUS IMAGING AGENTS

FILE REFERENCE: DTTI 113, JUSCI

CURRENT APPLICATION NUMBER: US/09/141.127A

CURRENT FILING DATE: 1998-08-27

EARLIER APPLICATION NUMBER: 08/3335, 832

EARLIER FILING DATE: 1995-01-05

EARLIER APPLICATION NUMBER: PCT/US93/04794

EARLIER FILING DATE: 1993-05-21

EARLIER APPLICATION NUMBER: 07/8866, 752

NUMBER OF SEQ ID NOs: 40

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 4

TYPE: PPT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

FEATURE:

NAME/KEY MOD RES

LOCATION: (1)

OTHER INFORMATION: BLOCKED: acetamidomethyl

FEATURE:

NAME/KEY MOD RES

LOCATION: (3)

OTHER INFORMATION: BLOCKED:acetamidomethyl

FEATURE:

NAME/KEY MOD RES

LOCATION: (1)

OTHER INFORMATION: BLOCKED: acetamidomethyl

FEATURE:

NAME/KEY MOD RES

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NAME/KEY MOD RES

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FEATURE:

NAME/KEY MOD RES

LOCATION: (3)

OTHER INFORMATION: BLOCKED:acetamidomethyl

FEATURE:

NAME/KEY MOD RES

LOCATION: (1)

OTHER INFORMATION: BLOCKED: acetamidomethyl

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/994,469A

FILING DATE: 21-DEC-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 551911man, F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 72-085-0 FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)413-3000

TELEFAX: (703)413-2220

TELEX: 243855 OPAT UR

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-07-994-469A-19

Query Match Score 26; DB 1; Length 14;

Best Local Similarity 58.3%; Prod. No. 6.7e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 RGDAAXGDSGP 12

Db 3 RGD-RGDSRAP 12

RESULT 7
PCT-US91-08328-35

SEQUENCE 35, Application PC/TUS9108328

GENERAL INFORMATION:

APPLICANT: Ruggeri, Zaverio M.

APPLICANT: Houghten, Richard A.

TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING

TITLE OF INVENTION: OF ADHESION MOLECULES

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN

STREET: 345 Park Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIF: 1015%

COMPILER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/08328

FILING DATE: 07-NOV-1990

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/610,363

ATTORNEY/AGENT INFORMATION:

NAME: Eugene Moroz

REGISTRATION NUMBER: 1511107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)758-4800

TELEFAX: (212)751-6849

RESULT 6
US-07-994-469A-19

SEQUENCE 19, Application US/07994469A

Patent No. 5519119

GENERAL INFORMATION:

APPLICANT: Yamada, No. 5519119utoshi

APPLICANT: Kato, Masanari

APPLICANT: Miyata, Keizo

APPLICANT: Aoyama, Yoshiyuki

APPLICANT: Shikama, Hiroshi

TITLE OF INVENTION: Polypeptide

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, P.C.

```

TELEX: 421792
SEQUENCE CHARACTERISTICS: 35:
LENGTH: 14 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE: NO
ANTI-SENSE: NO
NAME/KEY: Disulfide-bond
LOCATION: 1..>14
OTHER INFORMATION: /note= "Sequence linked by interchain disulfide bond at Cys residue with Cys residue on Arg8-Ser-Arg-Gly-Asp-Val-Cys"
OTHER INFORMATION: residue on Arg8-Ser-Arg-Gly-Asp-Val-Cys
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 4,683,291
FILING DATE: 28-OCT-1985
PUBLICATION DATE: 28-JUL-1987
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US B1 4,683,291
FILING DATE: 28-OCT-1985
PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-36
Query Match 36.6%; Score 26; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
PCT-US91-08328-35
Qy 1 RGDAC 5
Db 10 RGDVC 14

RESULT 9
PCT-US91-08328-37
Sequence 37, Application PC/TUS9108328
GENERAL INFORMATION:
APPLICANT: Ruggeri, Zaverio M.
APPLICANT: Houghton, Richard A.
TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08328
FILING DATE: 19911107
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Moroz, Eugene
REGISTRATION NUMBER: 25,237
PRIORITY NUMBER: US 07/610,363
FILING DATE: 07-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Moroz, Eugene
REGISTRATION NUMBER: 25,237
FILING DATE: 07-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Moroz, Eugene
REGISTRATION NUMBER: 1198 4079FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
MOLECULE TYPE: peptide
HYPOTHETICAL: NO

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ANTI-SENSE: NO
 FEATURE: Disulfide-bond
 LOCATION: 1..>14
 OTHER INFORMATION: /note= "Sequence linked by interchain disulfide bond at Cys residue with Cys residue on
 NAME KEY: Arg8-Leu-Arg-Gly-Asp-Val-Cys sequence"
 OTHER INFORMATION: residue on Arg8-Ala-Arg-Gly-Asp-Val-Cys sequence"
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: US 4,683,291
 FILING DATE: 28-OCT-1985
 PUBLICATION DATE: 28-JUL-1987
 DOCUMENT NUMBER: US B1 4,683,291
 FILING DATE: 28-OCT-1985
 PUBLICATION DATE: 03-JUL-1990
 PCT-US91-08328-38

Query Match 36.6%; Score 26; DB 5; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGDAC 5
 Db 10 RGDYC 14

RESULT 11
 US-08-441-507-43
 Sequence 43, Application US/08441507
 Patent No. 621458
 GENERAL INFORMATION:
 APPLICANT: Singh, Mohan Bir;
 APPLICANT: Smith, Penelope; and
 APPLICANT: Knox, Robert Bruce
 TITLE OF INVENTION: Protein Allergens of the Species Cynodon
 TITLE OF INVENTION: Proteins that inhibit platelet binding
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/441,507
 FILING DATE: 15-May-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/441,507
 FILING DATE: 30-October-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-049DV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 9
 OTHER INFORMATION: /note= "xaa is an unknown amino acid"
 Query Match 35.2%; Score 25; DB 3; Length 14;

ANTI-SENSE: NO
 FEATURE: Disulfide-bond
 LOCATION: 1..>14

Best Local Similarity 62.5%; Pred. No. 9.4e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
 US-08-441-507-49
 Sequence 49 Application US/08441507
 Patent No. 6214338
 GENERAL INFORMATION:
 APPLICANT: Singh, Mohan Bir;
 APPLICANT: Smith, Penelope; and
 APPLICANT: Knox, Robert Bruce
 TITLE OF INVENTION: Protein Allergens of the Species Cynodon
 TITLE OF INVENTION: Protein Allergens of the Species Cynodon
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTY: USA
 ZIP: 0109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/441,507
 FILING DATE: 15-May-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,875
 FILING DATE: 30-October-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Mantragorar, Amy E.
 REGISTRATION NUMBER: 36,207
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (617) 227-7400
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 9
 OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
 US-08-441-507-49
 Query Match 35.2%; Score 25; DB 4; Length 14;
 Best Local Similarity 62.5%; Pred. No. 9.4e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
 US-08-487-431-2
 Sequence 2 Application US/08487431
 Patent No. 5844050
 GENERAL INFORMATION:
 APPLICANT: Anderson, David C.
 APPLICANT: Mathews, Antony J.
 APPLICANT: Trimble, Stephen P.
 TITLE OF INVENTION: Modified Hemoglobin-like Compounds
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SomaGen, Inc.
 STREET: 2545 Central Avenue, Suite F01
 CITY: Boulder
 STATE: Colorado
 ZIP: 80301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.5
 SOFTWARE: Microsoft Word 5.0a
 CURRENT APPLICATION DATA:

RESULT 13
 US-07-969-875A-43
 Sequence 43 Application US/07969875A
 Patent No. 644157
 GENERAL INFORMATION:
 APPLICANT: Singh, Mohan Bir;

APPLICATION NUMBER: US/08/487,431
 FILING DATE: June 7, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/240,712
 FILING DATE: NO. 5844190ember 6, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Theresa A.
 REGISTRATION NUMBER: 32,547
 ATTORNEY/AGENT INFORMATION:
 NAME: Ramsey R. Stewart
 REGISTRATION NUMBER: 38,322
 REFERENCE/DOCKET NUMBER: 61
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303-511-3356
 TELEFAX: 303-444-3013
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14
 TYPE: amino acid
 TOPOLOGY: unknown to applicant
 MOLECULE TYPE: peptide
 HYPOTHETICAL: no
 US-08-487-431-2

Query Match 33.8%; Score 24; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 GDACXGDSGG 11
 Db 2 GGGSGSGG 11

RESULT 15
 US-08-973-629-2
 / Sequence 2, Application US/08973629A
 / GENERAL INFORMATION:
 / APPLICANT: Trimble, Stephen
 / APPLICANT: Mathews, Anthony
 / APPLICANT: Kerwin, Bruce
 / APPLICANT: Marguardt, David
 / APPLICANT: Anthony-Cahill, Spencer
 / APPLICANT: Epp, Janice
 / APPLICANT: Madril, Dominic
 / APPLICANT: Anderson, David
 / TITLE OF INVENTION: MODIFIED HEMOGLOBIN-LIKE COMPOUNDS AND METHODS OF
 / PURIFYING SAME
 / FILE REFERENCE: BXTB-1928
 / CURRENT APPLICATION NUMBER: US/08/973,629A
 / CURRENT FILING DATE: 1996-08-24
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 2
 / LENGTH: 14
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence : Peptide linker
 / Patent No. 6150506
 / OTHER INFORMATION: to couple dialpha domains
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Peptide linker
 / OTHER INFORMATION: to couple dialpha domains
 US-08-973-629-2

Query Match 33.8%; Score 24; DB 3; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 GDACXGDSGG 11

Result No.	Score	Query	Match	Length	DB ID	Description
1	28	19.9	25	2	S1396	hypothetical protein - proteo-tyrosine kinase; neuromedin U - com kD antigen 84K protein histone H2B.1, specific neuromedin U - chi cytolytic enterotoxin ATPase-beta chain heat shock protein
2	26	18.4	25	2	A3179	protein-tyrosine kinase; neuromedin U - com kD antigen 84K protein histone H2B.1, specific neuromedin U - chi cytolytic enterotoxin ATPase-beta chain heat shock protein
3	26	18.4	25	2	D42397	protein-tyrosine kinase (EC 2.7.1.112) src - African clawed frog (fragment)
4	26	18.4	25	2	S07770	protein-tyrosine kinase (EC 2.7.1.112) src - African clawed frog (fragment)
5	25	17.7	25	2	A48543	Xenopus laevis (African clawed frog)
6	25	17.7	25	2	A30590	Xenopus laevis (African clawed frog)
7	23	16.3	25	2	T01689	Xenopus laevis (African clawed frog)
8	23	16.3	25	2	A60807	Nucleic Acids Res. 13, 1747-1761, 1985
9	22	15.6	25	2	T09385	A;Title: Two divergent cellular src genes are expressed in Xenopus laevis.
10	22	15.6	25	2	S55765	A;Cross-references: GB:M30859; NID:G21481; PID:AA49964; 1; PMID:85215578; PMID:2987836
11	22	15.6	25	2	B85928	A;Reference number: 151563
12	22	15.6	25	2	I56918	A;Accession: I51565
13	21.5	15.2	25	2	A60741	A;Status: preliminary; translated from GB/EMBL/DDBJ
14	21.5	15.2	25	2	B20516	A;Residues: 1-25 <STE>
15	21	14.9	25	2	S26893	A;Cross-references: GB:M30859; NID:G21481; PID:AA49964; 1; PMID:85215578; PMID:2987836
16	21	14.9	25	2	JH0701	C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 domain; ATP; blocked amino end; lipoprotein; myristylation; phosphotransferease; tyrosine kinase; T-cell receptor beta chain; omega-conotoxin MVIIg heavy chain V ¹⁻²⁵
17	21	14.9	25	2	B41606	C;Keywords: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 domain; ATP; blocked amino end; lipoprotein; myristylation; phosphotransferease; tyrosine kinase; T-cell receptor beta chain; omega-conotoxin MVIIg heavy chain V ¹⁻²⁵
18	21	14.9	25	2	S22234	F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
19	20.5	14.5	25	2	B886074	Query Match 18.4%; Score 26; DB 2; Length 25;
20	20	14.2	25	2	A20396	Best Local Similarity 62.5%; Pred. No. 3.3e+03; Indels 0; Gaps 0;
21	20	14.2	25	2	B20516	Matches 5; Conservative 1; Mismatches 2;
22	20	14.2	25	2	JH0701	Query Match 18.4%; Score 26; DB 2; Length 25;
23	20	14.2	25	2	JH0700	Best Local Similarity 62.5%; Pred. No. 3.3e+03; Indels 0; Gaps 0;
24	20	14.2	25	2	PH1716	Matches 5; Conservative 1; Mismatches 2;
25	20	14.2	25	2	PH1910	Query 3 TRYKDEG 10
26	20	14.2	25	2	S03409	Db 4 TKSKEPREG 11
27	20	14.2	25	2	S10197	
28	20	14.2	25	2	S17633	
29	20	14.2	25	2	PH1907	

ALIGNMENTS

RESULT 1
 S1396 hypothetical protein - phage TW19 (fragment)
 C;Species: phage TW19
 C;Date: 18-Feb-1994 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
 C;Accession: S1396 R;Inokuchi, Y.; Hirashima, A.; Watanabe, I.
 J. Mol. Biol. 158, 711-730, 1982
 A;Title: Comparison of the nucleotide sequences at the 3'-terminal region of RNAs from R. A;Status: translation not shown
 A;Reference number: S1396 A;Accession: S1396 A;Molecule type: genomic RNA
 A;Residues: 1-25 <INQ>
 A;Cross-references: EMBL:J02520; NID:G216180
 Query Match 19.9%; Score 28; DB 2; Length 25;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03; Mismatches 2; Conservative 5; Indels 0; Gaps 0;
 Matches 9 EGKGDAGEG 18
 Qy :||| Db :||| 7 ERKKTPSCBG 16

RESULT 2
 I51565 protein-Tyrosine kinase (EC 2.7.1.112) src - African clawed frog (fragment)
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Mar-2000
 C;Accession: I51565 R;Steele, R.E.
 Nucleic Acids Res. 13, 1747-1761, 1985
 A;Title: Two divergent cellular src genes are expressed in Xenopus laevis.
 A;Cross-references: GB:M30859; NID:G21481; PID:AA49964; 1; PMID:85215578; PMID:2987836
 A;Reference number: 151563
 A;Accession: I51565
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Residues: 1-25 <STE>
 A;Cross-references: GB:M30859; NID:G21481; PID:AA49964; 1; PMID:85215578; PMID:2987836
 C;Keywords: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 domain; ATP; blocked amino end; lipoprotein; myristylation; phosphotransferease; tyrosine kinase; T-cell receptor beta chain; omega-conotoxin MVIIg heavy chain V¹⁻²⁵

RESULT 3
A34179 neuromedin U - common frog (common frog)
C;Species: Rana temporaria
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 18-Jun-1993
C;Accession: A34179
R;Domin, J.; Yiangou, Y.; Spokes, R.A.; Aitken, A.; Parmar, K.B.; Chrysanthou, B.J.; Biol. Chem. 264, 20881-20885, 1989
A;Title: The distribution, purification, and pharmacological action of an amphibian neuromedin U.
A;Reference number: A34179; MUID:90078173; PMID:2592357
A;Accession: A34179
A;Molecule type: protein
A;Residues: 1-25 <DOM>
A;Experimental source: small intestine
A;Note: sequence extracted from NCBI backbone (NCBIP:120483)

Query Match 18.4%; Score 26; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KPDEGKRG 13
Db 2 KPDEELOQ 9

RESULT 4
D42397 RU antigen 84K protein (fraction 15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Accession: D42397
R;Wedrychowski, A.; Henzel, W.; Huston, L.; Paslidis, N.; Ellerson, D.; McRae, M.; Seong J.; Biol. Chem. 267, 4533-4540, 1992
A;Title: Identification of proteins binding to interferon-inducible transcriptional enhancers
A;Reference number: A42397; MUID:92165807; PMID:15378319
A;Accession: D42397
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25 <WWD>
A;Experimental source: K562 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:85285)

Query Match 18.4%; Score 26; DB 2; Length 25;
Best Local Similarity 43.0%; Pred. No. 3.5e+03; Indels 2; Gaps 1;
Matches 7; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 9 EGKRGD-ACEGDGG 22
Db 1 DCPGSGTAAVFEEGG 16

RESULT 5
S07770 histone H2B.1, sperm - sea urchin (*Echinus esculentus*) (fragment)
C;Species: *Echinus esculentus*
C;Accession: S07770
R;Hill, C.S.; Thomas, J.O.
Biol. J. Biocom. 187, 145-153, 1990
A;Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal tail
A;Reference number: S07769; MUID:90126812; PMID:2298202
A;Molecule type: protein
A;Residues: 1-25 <HII>
C;Superfamily: histone H2B
C;Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 17.8%; Score 25; DB 2; Length 25;
Best Local Similarity 36.4%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TRYKPDGKGK 13
Db 12 TKRSPQKGK 22

RESULT 6
A45543 neuromedin U - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A45543
R;Domin, J.; Benito-Orfila, M.A.; Nandha, K.A.; Aitken, A.; Bloom, S.R.
Regul. Pept. 41, 1-8, 1992
A;Title: The purification and sequence analysis of an avian neuromedin U.
A;Reference number: A48543; MUID:93087774; PMID:1455013
A;Accession: A48543
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25 <DOM>
A;Experimental source: small intestine
A;Note: sequence extracted from NCBI backbone (NCBIP:120483)

Query Match 17.7%; Score 25; DB 2; Length 25;
Best Local Similarity 55.6%; Pred. No. 4.8e+03; Indels 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 YKEDDEGRG 13
Db 1 YKVEDDQG 9

RESULT 7
A30590 cytolytic enterotoxin - *Aeromonas hydrophila* (fragment)
C;Species: *Aeromonas hydrophila*
C;Accession: A30590
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 11-Jan-2000
R;Rose, J.M.; Houston, C.W.; Coppenhaver, D.H.; Dixon, J.D.; Kurosky, A.
Infect. Immun. 57, 1165-1169, 1989
A;Title: Purification and chemical characterization of a cholera toxin-cross-reactive C-terminal fragment of the cytolytic enterotoxin of *Aeromonas hydrophila*.
A;Reference number: A30590; MUID:89173315; PMID:2925244
A;Accession: A30590
A;Molecule type: protein
A;Residues: 1-25 <ROS>
C;Superfamily: aerolysin

Query Match 16.1%; Score 23; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 9e+03; Indels 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTRYKPY 7
Db 20 GDYXRP 25

RESULT 8
T01689 ATPase-beta chain - maize chloroplast (fragment)
C;Species: chloroplast Zea mays (maize)
C;Accession: T01689
R;Bradley, D.; Gatensby, A.A.
EMBO J. 4, 3641-3648, 1985
A;Title: Mutational analysis of the maize chloroplast beta subunit gene promoter system.
A;Reference number: Z14396; MUID:8613606; PMID:304965
A;Accession: T01689
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-25 <BRA>
A;Cross-references: EMBL:X03396; NID:gi12404; PIDN:CAA27131.1; PID:gi12405
A;Genome: chloroplast
C;Genetics:
C;Keywords: chloroplast

Query Match 16.3%; Score 23; DB 2; Length 25;

Best Local Similarity 35.7%; Pred. No. 9e+03; 1; Mismatches 8; Indels 0; Gaps 0; A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 <TUR>

Qy 4 RYKPDDEGKRGDACE 17
Db 2 RTNPTTSRPGDPLE 15

RESULT 9
A60807 heat shock protein 90 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: A60807
R;Denis, M.; Denis, R.; Deniz, M.
A;Title: Two-step purification and N-terminal amino acid sequence analysis of the rat M-
A;Reference number: A60807; MUID:83048319; PMID:3189818
A;Accession: A60807
A;Molecule type: Protein
A;Residues: 1-25 <DEN>
C;Comment: This protein associates with steroid hormone receptors and with the Rous sarco-
cytoma virus. It is also found in the heart, liver, lung, kidney, and testes.
C;Superfamily: heat shock protein 90
C;Keywords: Phosphoprotein

Query Match 15.6%; Score 22; DB 2; Length 25;
Best Local Similarity 37.5%; Pred. No. 1.2e+04; 1; Mismatches 4; Indels 0; Gaps 0;
Matches 3; Conservative 4; Gaps 0;
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE005174; NID:912517242; PIDN:AG57886.1; GSPDB:GN00145; UWGP:Z40
A;Accession: B85928

Qy 7 PDEGKRGD 14
Db 1 PEEVQKGE 8

RESULT 10
T09385 rev protein - human immunodeficiency virus type 1 (isolate cntri 1) (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09385
R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Marianni, R.; Busch, M.P.; Bir-
J. Virol., 69, 4228-4236, 1995
A;Reference number: Z16654; MUID:976982
A;Accession: T09385
A;Molecule type: DNA
A;Residues: 1-25 <MIC>
A;Cross-references: EMBL:U24451; NID:9829440; PIDN:AAA79577.1; PMID:9829445
C;Genetics:
A;Gene: rev
C;Superfamily: AIDS trans-regulatory splicing protein

Query Match 15.6%; Score 22; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.2e+04; 1; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 2; Gaps 0;
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25 <WNA>

Qy 10 GKRGDACE 17
Db 3 GRSGDSDE 10

RESULT 11
S55765 interferon-inducible protein 6-16 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C;Accession: S55765
R;Turri, M.G.; Cuiri, K.A.; Porter, A.C.G.
Nucleic Acids Res., 23, 1854-1861, 1995
A;Title: Characterisation of a novel minisatellite that provides multiple splice donor sites
A;Reference number: S55765; MUID:93319824; PMID:759609
A;Accession: S55765

Qy 1 AGTRYKPDDEGKR 12
Db 8 AGENAGKDAGRK 19

RESULT 12
B85928 hypothetical protein 24088 [imported] - Escherichia coli (strain O157:H7, substrate EDL9
C;Species: Escherichia coli
C;Accession: B85928
C;Sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimambato, E.; Potamitis, K.; Apodaca,
Nature, 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE005174; NID:912517242; PIDN:AG57886.1; GSPDB:GN00145; UWGP:Z40
A;Accession: B85928

Qy 5 YKPDEGKR 13
Db 9 YFEHEGLRG 17

Query Match 15.6%; Score 22; DB 2; Length 25;
Best Local Similarity 55.6%; Pred. No. 1.2e+04; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Gaps 0;
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE005174; NID:912517242; PIDN:AG57886.1; GSPDB:GN00145
A;Accession: B85928

Qy 5 YKPDEGKR 13
Db 9 YFEHEGLRG 17

Query Match 15.6%; Score 22; DB 2; Length 25;
Best Local Similarity 55.6%; Pred. No. 1.2e+04; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Gaps 0;
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE005174; NID:912517242; PIDN:AG57886.1; GSPDB:GN00145
A;Accession: B85928

Qy 5 YKPDEGKR 13
Db 9 YFEHEGLRG 17

Query Match 15.6%; Score 21.5%; DB 2; Length 25;
Best Local Similarity 41.7%; Pred. No. 1.4e+04; 1; Mismatches 4; Indels 1; Gaps 1;
Matches 5; Conservative 2; Gaps 1;

Qy 13 GD-ACGDGSGP 23
Db 1 GDTGAKGEKGHP 12

RESULT 14
A60741

insulin-like growth factor-binding protein He39L - human (Fragment)
 C;Species: Homo sapiens (man)
 C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
 C;Accession: A60741
 R;Forbes, B.; Ballard, P.J.; Walice, J.C.
 J.; Endocrinol 126, 497-506, 1990
 A;Title: An insulin-like growth factor-binding protein purified from medium conditioned
 A;Reference number: A60741; MUID:91011238; PMID:1698807
 A;Accession: A60741
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-25 <FOR>

Query Match 15.2%; Score 21.5; DB 2; Length 25;
 Best Local Similarity 33.3%; Pred. No. 1.4e+04;
 Matches 7; Conservative 2; Mismatches 7; Indels 5; Gaps 1;
 Qy 7 PDEGKR----GDAGEGDSGG 22
 :| :| | | |
 Db 5 PGQGVQAGKXPBGGXVEBEDRGG 25

RESULT 15

D26889
 T-cell receptor beta chain V-J-C regions (52H10F11) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 30-May-1997
 C;Accession: D26889
 R;Sherman, D.H.; Hochman, P.S.; Dick, R.; Tizard, R.; Ramachandran, K.L.; Flavell, R.A.;
 Mol Cell Biol 7, 1865-1872, 1987
 A;Title: Molecular analysis of antigen recognition by insulin-specific T-cell hybridomas
 A;Reference number: A26889; MUID:87257888; PMID:2439999
 A;Accession: D26889
 A;Molecule type: mRNA
 A;Residues: 1-25 <SHE>
 A;Cross-references: GB:M16121
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 14.9%; Score 21; DB 2; Length 25;
 Best Local Similarity 60.0%; Pred. No. 1.7e-04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 117 EGDSG 21
 :| :| :|
 Db 7 DGDTG 11

Search completed: February 26, 2004, 09:50:07
 Job time : 23 secs

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6					
In on:	February 26, 2004, 09:43:07 ; Search time 11 Seconds (without alignments)					
	118.341 Million cell updates/sec					
Title:	US-09-909-348-5					
Effect score:	141					
Sequence:	1 AGTRYPDCKRGIDACEGDSGGPPV 25					
Scoring table:	BLOSUM62					
Gapext:	0.5					
Total number of hits satisfying chosen parameters:	103					
Minimum DB seq length: 25						
Maximum DB seq length: 25						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing First 45 summaries						
Database :	SwissProt_42:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
	Query Match Length DB ID Description					
result No.	Score	Match	Length	DB	ID	
1	26	18.4	25	1	NEUJ_RANTE	P2056 rana tempor
2	25	17.7	25	1	BTI2_BOOMI	P83603 boophilus m
3	25	17.7	25	1	CYC4_VIBRI	P80891 vibrio fisc
4	25	17.7	25	1	H2B1_ECHBS	P34961 echinus esc
5	25	17.7	25	1	NEUJ_CHICK	P34963 Gallus galli
6	23	16.3	25	1	BOTR_BOTJA	P22028 bothrops ja
7	21	14.9	25	1	CXOB_CONCB	P56918 conus catus
8	20	14.2	25	1	CXOB_CONNA	P04485 conus magnus
9	20	14.2	25	1	K6P2_THETH	P17778 thermus the
10	20	14.2	25	1	TBA_TEPS	P21489 leptomonas
11	19	13.5	25	1	HCY3_MAISQ	P28304 maia squina
12	19	13.5	25	1	NEUJ_PIG	P23964 sus scrofa
13	19	13.5	25	1	VGJ_BPG4	P06652 bacriophila
14	18.5	13.1	25	1	MT_AGBBI	P03558 agaricus bi
15	18.5	13.1	25	1	MT_NEURCR	P02807 neurospora
16	18	12.8	25	1	BTI4_BOOMI	P83605 boophilus m
17	18	12.8	25	1	GBP_APAKA	P22800 apantelis k
18	18	12.8	25	1	LB01_BIOGL	P87472 bioluminesc
19	18	12.8	25	1	OM53_PORG1	P81363 porphyromon
20	18	12.8	25	1	Y194_ARCEU	P30045 archeoglob
21	17.5	12.4	25	1	FLAA_TREPA	P21183 treponema p
22	17	12.1	25	1	BGBP_PENVA	P81182 penaeus van
23	17	12.1	25	1	CPI2_SOLTU	P2744 solanum tub
24	17	12.1	25	1	CX6A_CONQU	P56843 conus querat
25	16	11.3	25	1	AHP3_ACICA	P83954 acinetobact
26	16	11.3	25	1	AMP3_MELGA	P8393 meleagris g
27	16	11.3	25	1	COX1_PARVE	Q01502 pracoccus
28	16	11.3	25	1	GLMK_PREBR	P8280 prevotella
29	16	11.3	25	1	IPYK_PSEAN	P8898 pseudanaba
30	16	11.3	25	1	LYC_ATRUE	P37715 asterias ru
31	16	11.3	25	1	SCRK_LACLA	Q91124 lactococcus
32	15	10.6	25	1	ANDT_ANNDU	P5684 androctonus
33	15	10.6	25	1	ATPD_NCTDU	P8285 microcconus
ALIGNMENTS						
RESULT 1						
NEUJ_RANTE						
ID P2056;						
STANDARD; PRT; 25 AA.						
AC 01-FEB-1991 (Rel. 17, Created)						
DT 01-FEB-1991 (Rel. 17, Last sequence update)						
DT 28-FEB-2003 (Rel. 41, Last annotation update)						
DE Neuromedin U-25 (NmU-25).						
OS Rana temporaria (European common frog);						
OC Bufo bufo; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.						
OX NCBI_TaxID=8457;						
RN [1]						
RP						
RC TISSUE=Intestine; RX MEDLINE=20078173; PubMed=2592357;						
RA Dom J., Yianguo Y.G., Spokes R.A., Aitken A., Parmar K.B., Chrysanthou B.J., Bloom S.R.;						
RA "The distribution, purification, and pharmacological action of an amphibian neuromedin U"; RT						
RL J. Biol. Chem. 264:12088-12095 (1989).						
CC -1- FUNCTION: Stimulates uterine smooth muscle contraction and causes selective vasoconstriction.						
CC -1- SIMILARITY: Belongs to the Nmu family.						
DR PIR: A34179; A34179.						
DR InterPro; IPR00119; NMU.						
DR Pfam; PF01070; NMU; 1.						
DR SMART; SM00084; NMU; 1.						
DR PROSITE; PS00967; NMU; 1.						
KW Amidation; Hormone.						
FT MOD_RES 25						
SQ SEQUENCE 25 AA; 2832 MW; 6A01D89FFDA06FD4 CRC64;						
OY 6 KPDEGKRG 13						
Db 2 KPDEFLQG 9						
RESULT 2						
BTI2_BOOMI						
ID BTI2_BOOMI						
AC P83605;						
DT 10-OCT-2003 (Rel. 42, Created)						
DT 10-OCT-2003 (Rel. 42, Last sequence update)						
DE Kunitz-type serine protease inhibitor BTI2-2 (Fragment).						
OS Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodida; Boophilus.						
OC						
RX NCBI_TaxID=6941;						
RN [1]						

SEQUENCE, AND FUNCTION.

RC STRAIN=ATCC 33715 / Y-1;
 RA Sasai S.D., Hirara I.Y., Tanaka A.S.;
 RT "Molecular studies of serine protease inhibitors from cattle tick
 Boophilus microplus (Larva).";
 RL Subunit (JUN-2003) (Rel. 13, Last sequence update)
 CC -!- FUNCTION: Inhibits trypsin, human plasma kallikrein and human
 neutrophil elastase.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR InterPro; IPR00222; Kunitz_BPTI.
 PROSITE; PS00280; BPTI_KUNITZ_1; PARTIAL.
 PROSITE; PS50279; BPTI_KUNITZ_2; PARTIAL.
 KW Serine protease inhibitor.
 ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
 FT NON TER 25 25 MW; DBE538C2C2B20466 CRC64;
 SQ SEQUENCE 25 AA; 2691 MW;

Query Match Score 25; DB 1; Length 25;
 Best Local Similarity 46.2%; Pred. No. 2.1e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 13 GDACE--GDSGGP 23
 Db 4 GPVCBLPKEVGGP 16

RESULT 3

CYCA_VIBFI STANDARD; PRT; 25 AA.

AC P80831; ID NBUU_CHICK STANDARD; PRT; 25 AA.

DT 15-JUL-1998 (Rel. 36, Created);
 DT 15-JUL-1998 (Rel. 36, Last sequence update);
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Putative cytochrome C4 (C551) (Fragment).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibionaceae; Vibrio.
 NCBI_TaxID=666;

RN SEQUENCE.

RC STRAIN=ATCC 33715 / Y-1;
 RX MEDLINE=97326008; PubMed=9183020;
 RA Petushkov V.N.; Lee J.;
 RT "Purification and characterization of flavoproteins and cytochromes
 from the yellow bioluminescence marine bacterium Vibrio Fischeri
 strain Y1.";
 RL Eur. J. Biochem. 245: 790-796 (1997).
 CC -!- FUNCTION: DIHENE, HIGH POTENTIAL CYTOCHROME C BELIEVED TO BE AN
 INTERMEDIATE ELECTRON DONOR TO TERMINAL OXIDATION SYSTEMS (BY
 SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -!- PTM: Binds two groups per molecule (By similarity).
 DR InterPro; IPR000345; CYC_heme_BS.
 DR PROSITE; PS00190; CYTOCHROME_C_1.
 FT BINDING 14 HEME 1 (COVALENT) (BY SIMILARITY).
 FT BINDING 17 HEME 1 (COVALENT) (BY SIMILARITY).
 FT UNSURE 14 14
 FT UNSURE 17 17
 FT NON TER 25 25 MW; CFBDD9A5933186C7 CRC64;

Query Match Score 25; DB 1; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2.1e+03; Indels 0; Gaps 0;

Qy 15 ACEGDGS 21
 Db 16 ACHGQEG 22

RESULT 4

H2B1_ECHES STANDARD; PRT; 25 AA.

AC H2B1_ECHES ID P13231; DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histone H2B.1, sperm (Fragment).
 OS Echinus esculentus (Sea Urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Eusynalloidea; Echinatea; Echinidae; Echinidae; Echinidae.
 NCBI_TaxID=7644;

RN [1] SEQUENCE.
 RX MEDLINE=90126812; PubMed=2298202;
 RA Hill C.S., Thomas J.O.;
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal tail of H2B interacts with linker DNA.";
 RL Eur. J. Biochem. 187:145-153 (1990).
 CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146 bp of DNA.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the histone H2B family.
 DR PIR: S07770; S07770;
 DR InterPro; IPR00558; Histone_H2B.
 DR PROSITE; PS00337; HISTONE_H2B; PARTIAL.
 KW Nucleolar protein; Chromosomal protein; Nucleosome core; DNA-binding; Nucleic acid binding; Multigene family.
 RN Multigene family.
 FT NON_TER 25 25 MW; 9842DD3D3A3A9EC CRC64;
 SQ SEQUENCE 25 AA; 2693 MW;

Query Match Score 25; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 2.1e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TRYKPPDGKRG 13
 Db 12 TKRSPQKGKRG 22

RESULT 5

NEUU_CHICK STANDARD; PRT; 25 AA.

AC P34933; ID NBUU_CHICK STANDARD; PRT; 25 AA.

DT 01-FEB-1994 (Rel. 28, Created);
 DT 01-FEB-1994 (Rel. 28, Last sequence update)

DE Neuromedin U-25 (NMU-25) [Contains: Neuromedin U-9 (NMU-9)].
 OC Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 NCBI_TaxID=9031;

RN [1] SEQUENCE.

RC TISSUE=Intestine; MEDLINE=92158816; PubMed=1788145;
 RX O'Harte F., Bockman C.S., Zeng W., Abel P.W., Harvey S., Conlon J.M.;
 RT "Primary structure and pharmacological activity of a nonapeptide related to neuromedin U isolated from chicken intestine.";
 RL Peptides 12:809-812 (1991).

CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes selective vasoconstriction.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NMU family.

DR PIR: A48543; R48543;
 DR InterPro; IPR008199; NMU.

DR Pfam; PF02070; NMU; 1.
 DR SMART; SMO084; NMU; 1.
 DR PROSITE; PS0967; NMU; 1.
 KW Amidation; Hormone.
 FT PEPTIDE 1 25 NEUROMEDIN U-25.
 FT PEPTIDE 17 25 NEUROMEDIN U-9.
 MOD RES 25 25 AMIDATION.
 SQ SEQUENCE 25 AA; 2921 MW; 54209DB487686B1A CRC64;
 Query Match Similarity 17.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 55.6%; Prd. No. 2.1e+03; Indels 0; Gaps 0;
 Matches 5; Conservative 3; Mismatches 1; Pairs 0;
 Qy 5 YKPDDEGRKG 13
 Db 1 YKVDBEDLQG 9

RESULT 6
 BOTR_BOTUA STANDARD; PRT; 25 AA.
 ID P22028;
 AC 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2003 (Rel. 42, Last annotation update)
 DE Botrocein (Platelet coagglutinin) (Fragment).
 OS Bothrops jararaca (Jabaracá).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidostauria; Squamata; Schleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Venom; MEDLINE=9112280; PubMed=1933206;
 RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
 RA Fukui H., Sugimoto M., Ruggeri Z.M.;
 RT "isolation and chemical characterization of two structurally and
 functionally distinct forms of botrocein, the platelet coagglutinin
 isolated from the venom of Bothrops jararaca.",
 RL Biochemistry 30:1957-1964 (1991).
 CC -!- FUNCTION: There are two distinct forms of the von Willebrand
 factor-dependent platelet coagglutinin. The dimeric form is
 34-times more active than the one-chain botrocein in promoting
 VWF binding to platelets.
 CC -!- SUBUNIT: Monomer Botrocein and VWF form a soluble complex.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains numerous intrachain disulfide bonds.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR InterPro: IPR001304; Lectin, C.
 DR PROSITE: PS00615; PARTIAL.
 DR PROSITE: PS50041; C_TYPE_LECTIN_1; PARTIAL.
 KW Glycoprotein.
 FT VARIANT 2 2 I -> V.
 FT NON TER 25 25 D25D9031A705CAF8 CRC64;
 SQ SEQUENCE 25 AA; 2655 MW; 2655 MW; D25D9031A705CAF8 CRC64;

Query Match Similarity 16.3%; Score 23; DB 1; Length 25;
 Best Local Similarity 38.5%; Prd. No. 3.9e+03; Indels 2; Gaps 1;
 Matches 5; Conservative 4; Mismatches 2; Pairs 0;

Qy 11 XRGDACEGGSGGP 23
 Db 13 EEEGEEC-DXGTP 23

RESULT 7
 CXOB_CONCT STANDARD; PRT; 25 AA.
 AC P591T8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DR Omega-conotoxin CVIB.
 OS Conus catus (Cat cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=101291;
 RN RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RX MEDLINE=2051930; PubMed=10938266;
 RA Lewis R.J., Nielsen K.J., Craik D.J.,oughnan M.L., Adams D.A.,
 RA Sharpe J.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
 RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F./
 RA "Novel omega-conotoxins from Conus catus discriminate among neuronal
 calcium channel subtypes."
 RL J. Biol. Chem. 275:35335-3544 (2000).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC) (By
 CC similarity). This toxin blocks N-, P-, and Q-type calcium
 CC channels.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin O-supergfamily. Omega-type
 CC family.
 KW Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;
 KW Calcium channel inhibitor; Amidation.
 FT DISURFID 16 BY SIMILARITY.
 FT DISURFID 8 BY SIMILARITY.
 FT DISURFID 15 BY SIMILARITY.
 FT MOD RES 25 BY SIMILARITY.
 SQ SEQUENCE 25 AA; 2717 MW; D41AE5PSAF09552 CRC64;
 Query Match Similarity 14.9%; Score 21; DB 1; Length 25;
 Best Local Similarity 60.0%; Pred. No. 7.2e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Pairs 0;

RESULT 8
 CXOB_CONNA STANDARD; PRT; 25 AA.
 ID CXOB_CONNA
 AC P04515;
 RN SEQUENCE.
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Omega-conotoxin MVIIIB (SNX-159).
 OS Conus magus (Magus cone).
 OC Bivalvia; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=6432;
 RN PIR; JH0701; JH0701.

DR Omega-conotoxin CVIB.
 OS Conus catus (Cat cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=101291;
 RN RP SEQUENCE.
 RX MEDLINE=87299637; PubMed=2441741;
 RA Oliveira B.M., Cruz L.J., de Santos V., Lecheminant G.W., Griffin D.,
 RA Zeikis R.D., McIntosh J.M., Galvean R., Varga J., Gray W.R.,
 RA Rivier J.E.;
 RT "Neuronal calcium channel antagonists. Discrimination between calcium
 channel subtypes using omega-conotoxin from Conus magus venom."
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin O-supergfamily. Omega-type
 CC family.
 DR PIR; JH0701; JH0701.

DR HSSP; P05184; IINV.
 DR Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;
 KW Calcium channel inhibitor; Amidation.

FT	DISULFID	1	16	RN [1]	RN SEQUENCE FROM N.A.; PubMed=1131738;
FT	DISULFID	8	20	RP RX	RP MEDLINE=8833393; Cross G.A.M.; RX Belloratto V.; Cross G.A.M.;
FT	DISULFID	15	25	RA	RA "Characterization of RNA transcripts from the alpha tubulin gene cluster of Leptomonas seymouri."
FT	MOD RES	25	25	RT	RT Nucleic Acids Res. 16:3455-3465(1988).
SQ	SEQUENCE	25 AA;	2626 MW;	RL	-!- FUNCTION: Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the alpha-chain and one at a nonexchangeable site on the beta-chain.
				CC	-!- SUBUNIT: Dimer of alpha and beta chains.
				CC	-!- SIMILARITY: Belongs to the tubulin family.
Query Match	Similarity	14.2%	Score 20; DB 1; Length 25;	CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/).
Best Local Matches	Similarity	60.0%	Pred. No. 9.8e+03; 0; Mismatches 2; Indels 0; Gaps 0;	CC	CC CC
Qy	14 DACEG 18			CC	CC DR EMBL: X07716; CA3A30544.1; -.
Db	14 DCCTG 18			CC	CC DR PIR; S03409; S03409.
				CC	CC DR InterPro; IPR00317; Tubulin.
				CC	CC DR InterPro; IPR03008; Tubulin_FtsZ.
				CC	CC DR PROSITE; PS00227; TUBULIN; PARTIAL.
				KW	KW Microtubule; GTP-binding.
				FT	FT NON_TER 25 AA; 2727 MW; A32ABD05D74E7BA4 CRC64;
				SQ	SEQUENCE 25 AA; 25 AA;
RESULT 9	K6P2_THETH	STANDARD;	PRT;	25 AA.	Query Match 14.2%; Score 20; DB 1; Length 25;
ID	K6P2_THETH	STANDARD;	PRT;	25 AA.	Best Local Similarity 75.0%; Pred. No. 9.8e+03;
ID	P21789	STANDARD;	PRT;	25 AA.	Mismatches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
AC	K6P2_THETH	STANDARD;	PRT;	25 AA.	CC
DT	01-MAY-1991 (Rel. 18, Created)				CC DR
DT	01-MAY-1991 (Rel. 18, Last sequence update)				DR
DT	10-OCT-2003 (Rel. 42, Last annotation update)				DR
DE	6-phosphofructokinase isozyme 2 (EC 2.7.1.11) (Phosphofructokinase-2)				DR
DE	(PFK2) (Phosphofructokinase 2) (Fragment).				DR
OS	Thermus thermophilus.				DR
OC	Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;				DR
OC	Thermus.				DR
OX	NCBI_TaxID=274;				DR
RN	[1]				DR
RP	SEQUENCE.				DR
RC	ATC / ATCC 27634;				DR
RX	MEDLINE=91124297; PubMed=1830879;				DR
RA	Xu J., Oshima T., Yoshida M.;				DR
RT	"Phosphoenopyruvate-insensitive phosphofructokinase isozyme from Thermus thermophilus HB8";				DR
RT	J. Biochem. 109:1199-203(1991).				DR
RL	CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.				DR
CC	-!- ENZYME REGULATION: IN CONTRAST WITH PFK1 THIS ENZYME IS NOT AFFECTED BY PHOSPHOENOPYRUVATE.				DR
CC	-!- PATHWAY: Key control step of glycolysis.				DR
CC	-!- SUBUNIT: Homotrimer.				DR
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.				DR
CC	-!- SIMILARITY: Belongs to the Phosphofructokinase family.				DR
DR	HAMAP: MF_00339; Last 1.				DR
DR	InterPro; IPR000023; Pfam; kinase.				DR
DR	Pfam; PF00365; PFK_1.				DR
DR	PROSITE; PS00433; PHOSPHOFRUCTOKINASE; PARTIAL.				DR
DR	Kinase; Transferase; Glycolysis; Multigene Family.				DR
KW	FT 25				DR
SQ	SEQUENCE 25 AA; 2575 MW; E7AEC8D6110EBAA46 CRC64;				DR
					DR
Query Match	Similarity	14.2%	Score 20; DB 1; Length 25;		DR
Best Local Matches	Similarity	80.0%	Pred. No. 9.8e+03; 0; Mismatches 1; Indels 0; Gaps 0;		DR
Qy	18 GDGG 22				DR
Db	11 GBSPG 15				DR
					DR
RESULT 10	TBA_LEAVE	STANDARD;	PRT;	25 AA.	DR
AC	P10489	STANDARD;	PRT;	25 AA.	DR
DT	01-JUL-1989 (Rel. 11, Created)				DR
DT	01-JUL-1989 (Rel. 11, Last sequence update)				DR
DT	15-JUL-1999 (Rel. 38, Last annotation update)				DR
DE	* Tubulin alpha chain (Fragment).				DR
OS	Leptomonads; Trypanosomatida; Kinetoplastida; Leptomonas.				DR
OC	Bukaryota; Euglenozoa; Leptomonadida; Leptomonas.				DR
NCBI_TaxID=5684;					DR

QY 13 GD-ACEGDS 20
DB 1 GDCGCGSAS 9

RESULT 15
ID MT_NEUCR STANDARD; PRT; 25 AA.
AC 202807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Metallothionein (MT).
GN CNT.
OS Neurospora crassa.
OC Fungi: Ascomycota; Pezizomycorina; Sordariomycetes;
OX Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86030247; PubMed=2932331;
RA Muenger K., Germann U.A., Lerch K.;
RT "Isolation and structural organization of the Neurospora crassa
copper metallothionein gene.";
RL EMBO J. 4:2665-2668(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9112714; PubMed=2148862;
RA Romeyer F.M., Jacobs F.A., Brousseau R.;
RT "Expression of a Neurospora crassa metallothionein and its variants
in Escherichia coli.";
RL Appl. Environ. Microbiol. 56:2748-2754(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=8803908; PubMed=2959528;
RA Muenger K., Germann U.A., Lerch K.;
RT "Isolation and regulation of expression of the Neurospora crassa
copper metallothionein gene.";
RL Experientia Suppl. 52:393-400(1987).
RN [4]
RP SEQUENCE
RX MEDLINE=80143244; PubMed=644697;
RA Lerch K.;
RT "Copper metallothionein, a copper-binding protein from Neurospora
crassa";
RL Nature 284:368-370(1980).
RN [5]
RP STRUCTURE BY NMR
RX MEDLINE=89302887; PubMed=2525920;
RA Malikavil J.A., Lerch K., Armistage I.M.;
RT "Proton NMR studies of a metallothionein from Neurospora crassa:
sequence-specific assignments by NOE measurements in the rotating
frame.";
RL Biochemistry 28:2991-2995(1989).
CC -!- INDUCTION: By copper.
CC -!- MISCELLANEOUS: The seven cysteines bind six copper (cuprous) ions.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 8.

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or send an email to license@isb-sib.ch).

CC DR X03009; CA226793; 1; -
CC DR EMBL; NS9836; AA33594; 1; -
CC DR EMBL; N27703; AA33595; 1; -
CC PIR; A24641; SNNC.
KW Metal-binding: Metal-thiolate cluster; Copper.
CC INIT_MET 0 0 COPPER.
FT 3 3 COPPER.

Q9PXH2	PRELIMINARY;	PRT;	25 AA.	
Q9PXH2; ID: Q9PXH2; DT: 01-MAY-2000 (TREMBlrel. 13, Created)				
DT: 01-JUN-2003 (TREMBlrel. 13, Last sequence update)				
Variant transactivation factor (Fragment).				
Human T-lymphotropic virus 1.				
Viruses; Retroviridae; Retroviridae; Deltaretrovirus.				
[1]				
SEQUENCE FROM N.A.				
NEWIESK S., Daenke S., Parter C.E., Taylor G., Weber J., Nightingale S., Bangham C.R.; "Naturally occurring variants of human T-cell leukemia virus type I tax protein impair its recognition by cytotoxic T lymphocytes and the transactivation function of Tax." J. Virol. 69:2649-2653(1995); GO: GO:0016563; Pitranscriptional activator activity; IEA.				
GO: GO:0045941; Positive regulation of transcription; IEA.				
InterPro: IPR004120; TAX.				
Pfam; PF02959; TAX; 1. SEQUENCE 25 AA; 2638 MW; CF0FB4DDBB51D26 CRC64;				
Query Match Score 29; DB 15; Length 25; Best Local Similarity 50.0%; Pred. No. 3.2e+03; Indels 1; Gaps 1; Mismatches 2; Conservative 7; Matches 13; GDAEGD---SGG 22				
Qy : : Db 1 GDCYQGDWCFVSGG 14				
RESULT 3 Q9C5B6 PRELIMINARY; PRT;	25 AA.			
Q9C5B6; ID: Q9C5B6; DT: 01-JUN-2001 (TREMBlrel. 17, Created)				
DT: 01-JUN-2001 (TREMBlrel. 17, Last sequence update)				
01-JULY-2001 (TREMBlrel. 17, Last annotation update)				
Proline biosynthesis enzyme (Fragment).				
Arabidopsis thaliana (Mouse-ear cress).				
Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Arabidopsis.				
[1]				
SEQUENCE FROM N.A.				
Avila C.; "Genes responding to phosphate starvation placed together in Arabidopsis genome."; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
EMBL: AU275979; CAC35357.1; NON_TER 1. SEQUENCE 25 AA; 2712 MW; D3A469F94BSD36 CRC64;				
Query Match Score 28; DB 10; Length 25; Best Local Similarity 40.0%; Pred. No. 4.5e+03; Indels 3; Mismatches 3; Conservative 4; Matches 12; RGDACBDGSG 21				
Qy : : : : : : Db 4 KGQVYVBDGNG 13				
RESULT 4 Q42056 PRELIMINARY; PRT;	25 AA.			
Q42056; ID: Q42056; DT: 01-NOV-1996 (TREMBlrel. 01, Created)				
DT: 01-NOV-1996 (TREMBlrel. 01, Last sequence update)				
01-OCT-2002 (TREMBlrel. 22, Last annotation update)				
Glycine-rich RNA binding protein (Fragment).				
DE				
SEQUENCE FROM N.A.				
STRAIN: N.Cv. Columbia; Phillipps G., Gagot C.; Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.				
RC: STRAIN: N.Cv. Columbia; Phillipps G., Gagot C.; Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.				
RN: NCBI_TaxID:3702;				
RP: SEQUENCE FROM N.A.				
RC: STRAIN: N.Cv. Columbia; Phillipps G., Gagot C.; Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.				
RN: NCBI_TaxID:3702;				
FT: NON_TER 1. SEQUENCE 25 AA; 2421 MW; B1064170E1B33751 CRC64;				
Qy 18 GBSSGGPF 24				
Db 19 GDCGGGF 25				
RESULT 5 Q47669 PRELIMINARY; PRT;	25 AA.			
Q47669; ID: Q47669; DT: 01-NOV-1996 (TREMBlrel. 01, Created)				
DT: 01-NOV-1996 (TREMBlrel. 01, Last sequence update)				
01-DBC-2001 (TREMBlrel. 19, Last annotation update)				
TRPA46-ASP-PR3 protein (Fragment).				
DE: TRPA46-ASP-PR3				
GN: TRPA46-ASP-PR3				
OS: Escherichia coli.				
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.				
OC: Escherichia coli.				
NCBI_TaxID:562;				
OX: OX				
RN: RN				
RP: SEQUENCE FROM N.A.				
RC: STRAIN=K-12;				
RX: MEDLINE=893343228; PubMed=2502189;				
RA: Tucker S.D.; Murciano E.J.; Page1 F.T.; RT: "Missense and nonsense suppressors can correct frameshift mutations.";				
RT: "Missense and nonsense suppressors can correct frameshift mutations.";				
RL: Blockhine TL:729-739(1989).				
DR: X16698; CA34671.1; -.				
FT: NON_TER 1. SEQUENCE 25 AA; 2759 MW; 93B6A5FDAE24C8DB CRC64;				
Qy 5 YKPDEGKRGD 14				
Db 16 FRPGSGKSDD 25				
RESULT 6 Q16498 PRELIMINARY; PRT;	25 AA.			
Q16498; ID: Q16498; DT: 01-NOV-1996 (TREMBlrel. 01, Created)				
DT: 01-NOV-1996 (TREMBlrel. 01, Last sequence update)				
01-TUN-2003 (TREMBlrel. 24, Last annotation update)				
DE: GM-CSF receptor alpha subunit (Fragment).				
GN: CSFRA.				
OS: Homo sapiens (Human).				
OC: EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID:9616;				
RN: RN				
RP: SEQUENCE FROM N.A.				
RX: MEDLINE=31053200; PubMed=1158805;				
RA: Rapoport G., Willison T.A., Henke A., Gough N.M.;				

"Arrangement and localization of the human GM-CSF receptor alpha chain gene CSF2RA within the X-Y pseudoautosomal region.";
Genomics 14:455-461 (1992).

RT gene CSF2RA within the X-Y pseudoautosomal region.; IEA.
RL Genomics 14:455-461 (1992).
ID GO:0045941; P:transcriptional activator activity; IEA.

DR GO:0004872; F:receptor activity; IEA.

KW Receptor.;

FT 25 ;

SEQUENCE 25 AA; 3014 MW; 3A5827B3BF28E35E CRC64;

Query Match 19.1%; Score 27; DB 4; Length 25;

Best Local Similarity 57.1%; Pred. No. 6.3e+03; 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 YKPDDEGK 11

Db 6 FPPPEGK 12

RESULT 7

Q99148 PRELIMINARY; PRT; 25 AA.

ID Q99148 PRELIMINARY; PRT; 25 AA.

AC 069148 PRELIMINARY; PRT; 25 AA.

DT 01-NOV-1996 (TREMBLrel. 01; Created)

DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21; Last annotation update)

DE 61 Protein (Fragment).

DN WI.

OS Human herpesvirus 4 (Epstein-Barr virus).

OC dsDNA viruses; no RNA stage; Herpesviridae;

OC gammaherpesvirus; Lymphocryptoviridae.

OX NCBI_TaxID=10376;

RP SEQUENCE FROM N.A. NCBI_TaxID=10376;

RX MEDLINE=89030826; PubMed=2845663;

RX Sauter M., Boos H., Hirschi F., Mueller-Lantzsch N.;

RT "Characterization of a Latent Protein Encoded by the Large Internal

RT Repeats and the BamHI Y Fragment of the Epstein-Barr (EBV) Genome.";

DR Virology 166:1586-1590 (1988);

DR EMBL: M23259; AA045901; -;

DR InterPro; IPR005330; Herpes_LP.

DR PFM; PF03363; Herpes_LP; 1.

FT 25 AA; 2443 MW; 32530A494688E13 CRC64;

SEQUENCE 25 AA; Conservation 58.3%; Pred. No. 6.3e+03; 0; Mismatches 3; Indels 2; Gaps 1;

Query Match 19.1%; Score 27; DB 12; Length 25;

Best Local Similarity 58.3%; Pred. No. 6.3e+03; 0; Mismatches 3; Indels 2; Gaps 1;

Qy 12 RGDAACEGBGGP 23

Db 1 RGDRSEGB--GP 10

RESULT 8

Q9PXH3 PRELIMINARY; PRT; 25 AA.

ID Q9PXH3 PRELIMINARY; PRT; 25 AA.

AC Q9PXH3 PRELIMINARY; PRT; 25 AA.

DT 01-MAY-2000 (TREMBLrel. 13; Created)

DT 01-JUN-2003 (TREMBLrel. 13; Last sequence update)

OS Human T-lymphotropic virus 1.

OC Viruses; Retroviridae; Deltaretrovirus.

OX NCBI_TaxID=11908;

RN SEQUENCE FROM N.A. MEDLINE=95191051; PubMed=7533860;

RA Niewiesk S., Daenke S., Parker C.E., Taylor G., Weber J., Nightingale S., Bangham C.R.;

RA "Naturally occurring variants of human T-cell leukemia virus type I Tax protein impair its recognition by cytotoxic T lymphocytes and transactivation function of Tax.";

RT J. Virol. 69:2649-2653 (1995).

RT gene GO:0016563; P:transcriptional activator activity; IEA.
RL GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR04120; Tax.

DR Pfam; PF02955; Tax; 1.

DR SEQUENCE 25 AA; 2712 MW; 950FBDBBB5155F CRC64;

Query Match 19.1%; Score 27; DB 15; Length 25;

Best Local Similarity 50.0%; Prd. No. 6.3e+03; 1; Mismatches 2; Indels 4; Gaps 1;

Qy 13 GDAGEGD----SGG 22

Db 1 GDYVQGDNCPISSG 14

RESULT 9

Q07916 PRELIMINARY; PRT; 25 AA.

ID Q07916 PRELIMINARY; PRT; 25 AA.

AC 007916 (TREMBLrel. 04; Created)

DT 01-JUL-1997 (TREMBLrel. 04; Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)

DE Hypothetical protein.

OS Mycobacterium tuberculosis, and

OS Mycobacterium bovis BCG.

OC Bacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773; 33829;

RN SEQUENCE FROM N.A.

RC STRAIN=2296207, and PASTEUR;

RA SUPPLY_P.; Magdalena S., Impens S., Locht C.;

RL Submitted (20N1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; Y13628; CAA39601;

DR EMBL; Y13627; CAA39551;

DR EMBL; Y13628; CAA39591; -.

KW Hypothetical protein.

SEQUENCE 25 AA; 2633 MW; 036E7271A33D1CF2 CRC64;

Query Match 18.4%; Score 26; DB 2; Length 25;

Best Local Similarity 33.3%; Prd. No. 8.8e+03; 3; Mismatches 3; Indels 6; Gaps 1;

Qy 8 DEGRKGD----ACEGD 19

Db 6 DDAERSDEVGAPPAGGE 23

RESULT 10

Q9UQ00 PRELIMINARY; PRT; 25 AA.

ID Q9UQ00 PRELIMINARY; PRT; 25 AA.

AC Q9UQ00 PRELIMINARY; PRT; 25 AA.

DT 01-MAY-2000 (TREMBLrel. 13; Created)

DT 01-NAY-2000 (TREMBLrel. 13; Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9636;

RN SEQUENCE.

RX MEDLINE=21165807; PubMed=1537839;

RA Wedrychowski A., Henzel W., Huston L., Paslidis N., Ellerson D., McRae M.; Seong D., Howard O.M.; Deiseroth A.;

RA "Identification of proteins binding to interferon-inducible transcriptional enhancers in hematopoietic cells.";

RL J. Biol. Chem. 267:4533-4540 (1992).

DR PIR: D42397; D42397.

DR GO:0003677; F:DNA binding; NAS.

FT NON_TER 1

FT NON_TER 25

FT SEQUENCE 25 AA; 2550 MW; 997649686105DC69 CRC64;

ID 077828 PRELIMINARY; PRT; 25 AA.
 AC 077828;
 DT 01-NOV-1998 (TRIMBLref). 08; Created
 DT 01-NOV-1998 (TRIMBLref). 08; Last sequence update
 DT 01-OCT-2001 (TRIMBLref). 18; Last annotation update
 DE Testis specific protein (Fragment)
 OS Cercocobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Mammalia; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Etheridae; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercocebus;
 OX NCBI_TaxID:9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:CTL941, CTL926, CTA078, and F105;
 RA HARRIS E.E., DISCELLI T.R.;
 RT "Nuclear Gene Trees and the Phylogenetic Relationships of the
 Mangabeys (Primates: Papionini)." ;
 RF Mol. Biol. Evol. 0:0-0(1998).
 RL AF057414; AAC25142.1;
 DR EMBL; AF057414; AAC25142.1;
 DR EMBL; AF057411; AAC25139.1;
 DR EMBL; AF057412; AAC25140.1;
 DR AF057413; AAC25141.1;
 FT NON-TER 1 1
 FT NON-TER 25 25
 SEQUENCE 25 AA; 2799 MW; A50DACTA60359098 CRC64;
 Query Match 18.4%; Score 26; DB 6; Length 25;
 Best Local Similarity 37.5%; Pred. No. 8.8e+03;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Qy 6 KPDGKRDACEBDSG 21
 Db 1 KPHLDRRGATIQGMPG 16

Search completed: February 26, 2004, 09:49:36
 Job time : 42 secs

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4 protein - protein search, using sw model
on: February 26, 2004, 09:42:37 ; Search time 51 Seconds
(without alignment) 138 504 Million cell

title: US-99-909-348-5
perfect score: 141
sequence: 1 AGTRYKDEGKRGADECSDGGPFV 25

scoring table: BLOSUM62 Gapopen 10.0 , Gapext 0.5
 searched: 1586107 seqs, 282547505 residues
 total number of hits satisfying chosen parameters:

minimum DB seq length: 25
maximum DB seq length: 25

post-processing: Minimum Match 0%

ALIGNMENTS

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post-processing: Minimum Match 0%
                  Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseed_29Jan04:*
  1: geneseqp1980s:*
  2: geneseqp1990s:*
  3: geneseqp2000s:*
  4: geneseqp2001s:*
  5: geneseqp2002s:*
  6: geneseqp2003as:*
  7: geneseqp2003bs:*
  8: geneseqp2004s:*

```

Pred. No. is the number of results predicted score greater than or equal to the score of 1 and is derived by analysis of the total score

Result No.	Score	Query		Match Length	DB ID	Description
		No.	Peptide #			
1	36	25.5	AAM17856	25	4	Aam17856 Peptide #
2	36	25.5	AB33 6874	25	4	Abb336874 Peptide #
3	36	25.5	AAM3 0362	25	4	Aam30362 Peptide #
4	36	25.5	ABB3 1661	25	4	Abb31661 Peptide #
5	36	25.5	ABP2 2200	25	4	Abb2200 Protein #
6	36	25.5	AAM7 0024	25	4	Aam70024 Human bon
7	36	25.5	AAM5 7620	25	4	Aam57620 Human bra
8	36	25.5	ABG5 1720	25	4	Abg51720 Human liv
9	36	25.5	AAM0 5503	25	4	Aam05503 Peptide #
10	36	25.5	ABG3 9654	25	5	Abg39654 Human pep
11	34	24.1	AAGG 6984	25	4	Aag6984 Mutant pr
12	33	23.4	ABP3 8532	25	4	Abb38532 Peptide #
13	33	23.4	AAM3 1981	25	4	Aam31981 Peptide #
14	33	23.4	AAM7 1690	25	4	Aam71690 Human bon
15	33	23.4	AAM5 1914	25	4	Aam51914 Human liv
16	33	23.4	ABG5 3374	25	4	Abg53374 Human liv
17	33	23.4	ABG4 1503	25	5	Abg41503 Human pep
18	31.5	22.3	ADC9 3935	25	7	Adc93935 Peptide I
19	31	22.0	AAU9 0331	25	5	Aau90331 Insulin/I
20	31	22.0	ADP0 4468	25	6	Ada04468 IGF-1R re
21	30	21.3	AAP4 0290	25	2	Aap40290 Human con
22	30	21.3	AAT0 6185	25	2	Aat06185 Anti-angi
23	30	21.3	AAN8 8795	25	2	Aan88795 Polypeptid
24	30	21.3	ABBP 0650	25	4	Abb0650 Human sec
			ABD0 1550	25	5	Abd01550 Growth hor

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ESTIMATES

Result No.	Score	Query	Match	Length	DB ID	Description
		No.				
1	36	25.5	25	4	AAM17856	Aam17856 Peptide #
2	36	25.5	25	4	AB33 6874	Abb336874 Peptide #
3	36	25.5	25	4	AAM3 0362	Aam30362 Peptide #
4	36	25.5	25	4	ABB3 1661	Abb31661 Peptide #
5	36	25.5	25	4	ABB2 2200	Abb22200 Protein #
6	36	25.5	25	4	AAM7 0024	Aam70024 Human bon
7	36	25.5	25	4	AAM5 7620	Aam57620 Human bra
8	36	25.5	25	4	ABG5 1720	Abg51720 Human liv
9	36	25.5	25	4	AAM0 5503	Aam05503 Peptide #
10	36	25.5	25	5	ABG3 9654	Abg39654 Human pep
11	34	24.1	25	4	AAGG 6984	Aag6984 Mutant pr
12	33	23.4	25	4	ABB3 8532	Abb38532 Peptide #
13	33	23.4	25	4	AAM3 1981	Aam31981 Peptide #
14	33	23.4	25	4	AAM7 1690	Aam71690 Human bon
15	33	23.4	25	4	AAM5 1914	Aam51914 Human liv
16	33	23.4	25	4	ABG5 3374	Abg53374 Human liv
17	33	23.4	25	5	ABG4 1503	Abg41503 Human pep
18	31.5	22.3	25	7	ADC9 3935	Adc93935 Peptide I
19	31	22.0	25	5	AAU9 0631	Aau90631 Insulin/I
20	31	22.0	25	6	ADP0 4468	Adp04468 IGF-1R re
21	30	21.3	25	2	AAP4 0290	Aap40290 Human con
22	30	21.3	25	2	AAY0 6185	Aay06185 Anti-angi
23	30	21.3	25	2	AAW8 8795	Aaw88795 Polypeptid
24	30	21.3	25	4	ABB1 0650	Abb10650 Human sec
25	30	21.3	25	5	ABD1 1503	Abd11503 Growth hor

The present invention relates to human single exon nucleic acid probes (SENPs; see AAI0068-AAI459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa Cells. The sequence can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Moreover, the sequence can be used as a marker for cervical cancer.

16	21.3	2.5	6	ABO14907	Novel hum
17	21.3	2.5	7	ABO23887	Protein a
18	20.6	1	1	AAP293093	CD4 anti-
19	20.6	2	2	AAR29065	Generic P
20	20.6	2	2	AAR51963	Linker Pe
21	20.6	2	2	AAW10259	Haptitis
22	20.6	1	1	Aaw97179	Linker us
23	20.6	2	2	AAY9179	Single ch
24	20.6	2	2	AAY05761	Fragment
25	20.6	2	2	AAY36640	Aay36640
26	20.6	4	4	AM50156	MAB 9A4 s
27	20.6	6	6	AAC016697	Anti-ovar
28	20.6	6	6	AAC016508	Synthetic
29	20.6	6	6	ADA11881	Human nov
30	20.6	2	2	Aaw52207	Interleuk
31	20.6	2	2	Aaw91114	Human leu
32	20.6	2	2	Aaw8292	Fragment
33	20.6	4	4	Abz43355	Peptide #
34	20.6	4	4	Aam37208	Peptide #
35	20.6	4	4	Aam77088	Human bon
36	20.6	4	4	Aac07555	Human pol
37	20.6	4	4	AAA00556	Human

RESULT 1
 AAM17856
 ID AAM17856 standard; protein; 25 AA
 XX
 AC AAM17856;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Peptide #4290 encoded by Probe foo

Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer.

Homo sapiens:

WC200157278-A2

09-AHIG-2001

30-TIAN-2001 : 2001W0-IIS000670

04 - FEB - 2000 : 2000011S-0180312B

~~28 - MAI - 2000;~~ ~~20000US - 020/438P.~~
~~30 - JUN - 2000;~~ ~~20000US - 00608408~~

U3 -AUG-2000; 2000US=00832388.
31 -SEB-2000; 2000TS=0234687B

Z / -3EF = 2000 ; 2000G3 = 0238333E .
04 = OCT = 3000 ; 2000GB = 00034263

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG Hanzel DK Chen W

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human normal and tumor tissue. WPI; 2001-488901/53.

CC Part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp://wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 25 AA;
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACEGDSGGP 23
 DB : |||
 Ds 11 ACQSRSGGP 19

RESULT 2
 ABB36874 2
 ID ABB36874 standard; peptide; 25 AA.
 XX
 AC ABB36874;
 XX DT 04-FEB-2002 (first entry)
 XX Peptide #4380 encoded by human foetal liver single exon probe.
 XX Human: foetal liver; gene expression; single exon nucleic acid probe.
 KW XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000663.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-01756P.
 PR 30-JUN-2000; 2000US-01608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234587P.
 PR 27-SEP-2000; 2000US-0236339P.
 PR 04-OCT-2000; 2000GB-0002263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488897/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 CC gene expression in human Placenta.
 CC Claim 27; SEQ ID NO 30631; 654pp; English.
 CC The present invention relates to single exon nucleic acid probes (SENPs;
 CC see <http://www.ncbi.nlm.nih.gov/entrez/pmc/articles/131315/>). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.

SQ Sequence 25 AA;
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACEGDSGGP 23
 DB : |||
 Ds 11 ACQSRSGGP 19

RESULT 4
 ABB31661 4
 ID ABB31661 standard; peptide; 25 AA.
 XX
 AC ABB31661;
 XX DT 01-FEB-2002 (first entry)
 XX Peptide #4312 encoded by breast cell single exon nucleic acid probe.
 XX Human: microarray; single exon probe; gene expression; breast; disease;
 XX
 OS Homo sapiens.

SQ Sequence 25 AA;
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACEGDSGGP 23
 DB : |||
 Ds 11 ACQSRSGGP 19

PN WO200157271-A2.
 XX PD 09-AUG-2001.
 XX XX 30-JAN-2001; 2001WO-US000662.
 XX PF 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0068408.
 PR 03-AUG-2000; 2000US-0062366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0234359P.
 PR 04-OCT-2000; 2000US-0234263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-48899/53.
 XX PS Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX PS Claim 15; SEQ ID NO 23970; 530pp; English.
 XX CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC AB21535; ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosis diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC specification, at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 25 AA:
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 ID AAM70024 standard; protein: 25 AA.
 XX AC AAM70024;
 XX DT 06-NOV-2001 (first entry)
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30330.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX OS Homo sapiens.
 XX PN WO200157276-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000662.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0234687P.
 PR 03-AUG-2000; 2000US-0062366.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-48899/53.
 XX PS Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX PS Claim 15; SEQ ID NO 23970; 530pp; English.
 XX CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC AB21535; ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosis diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC specification, at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 25 AA:
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 ID AAM70024 standard; protein: 25 AA.
 XX AC AAM70024;
 XX DT 06-NOV-2001 (first entry)
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30330.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX OS Homo sapiens.
 XX PN WO200157276-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000662.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0234687P.
 PR 03-AUG-2000; 2000US-0062366.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0234359P.
 PR 04-OCT-2000; 2000GB-0002463.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI: 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX Example 4; SEQ ID NO 30330; 658pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX Sequence 25 AA;
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 ACEGDBGGP 23
 DB 11 ACQSRSGGP 19

RESULT 8
 ABG51720
 ID ABG51720 standard; peptide; 25 AA.
 XX
 AC ABG51720;
 XX DT 25-FEB-2003 (first entry)
 XX DB Human liver peptide, SEQ ID No 30368.
 XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 XX KW hypercholesterolaemia; coronary heart disease.
 XX Homo sapiens.
 OS
 XX PN WO200157223-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 20001WO-US000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 DE 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 KW PR 03-AUG-2000; 2000US-00612366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0233359P.
 PR 04-OCT-2000; 2000GB-00034263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PI WPI: 2001-488900/53.
 XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX Claim 27; SEQ ID NO 30368; 658pp; English.
 XX The invention relates to a single exon nucleic acid probe (SEN1) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (II) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinemia, hypercholesterolemia which is
 CC associated with coronary heart disease. ABG51720/ABG51930 repress human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

PR 30-JAN-2001; 20001WO-US000667.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00612366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0233359P.
 PR 04-OCT-2000; 2000GB-00034263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI: 2001-483446/52.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX Example 4; SEQ ID NO 29725; 650pp + Sequence Listing; English.
 XX PS

XX	SQ Sequence 25 AA;	Db	11 : 19
Query Match 25.5% ; Score 36 ; DB 4 ; Length 25 ; Best Local Similarity 6.7% ; Pred. No. 1.9e+03 ; Matches 6 ; Conservative 1 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;			
QY 15 ACEGDSGGP 23 Db 11 ACQSRSGGP 19			
RESULT 9			
AAMM5503 ID AAMM5503 standard; protein; 25 AA.			
XX AC AAMM5503 ; XX DT 09-OCT-2001 (first entry)			
Peptide #4185 encoded by probe for measuring breast gene expression. Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour. Homo sapiens.			
XX PN WO200152270-A2.			
PD 09-AUG-2001.			
XX PF 29-JAN-2001; 2001WO-US000661.			
XX PR 04-FEB-2000; 2000US-0180312P. PR 26-MAY-2000; 2000US-0207456P. PR 30-JUN-2000; 2000US-0068408. PR 03-AUG-2000; 2000US-00632366. PR 21-SEP-2000; 2000US-0214687P. PR 27-SEP-2000; 2000US-0234687P. PR 04-OCT-2000; 2000US-0023359P. PR 04-OCT-2000; 2000GB-00024263.			
XX (MOLE-) MOLECULAR DYNAMICS INC.			
PA PI Penn SG, Hanzel DK, Chen W, Rank DR; XX DR WPI; 2001-47286/51.			
XX Novel single exon nucleic acid probe used to measuring gene expression in a human breast.			
PT PS Claim 27; SEQ ID NO 14243; 322PP; English.			
XX The present invention relates to novel single exon nucleic acid probes (see At 00010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosis diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocytic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ipo.int/pub/published_pct_sequences			
XX Sequence 25 AA;			
SQ Query Match 25.5% ; Score 36 ; DB 4 ; Length 25 ; Best Local Similarity 6.7% ; Pred. No. 1.9e+03 ; Matches 6 ; Conservative 1 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;			
QY 15 ACEGDSGGP 23			

the exons should be assigned to a single gene; a peptide comprising one of 12/11 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Kaposi's syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

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Sequence 25 AA;
Query Match      25.5%; Score 36; DB 5; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0;
Gaps 0;
15 ACEGDSSGP 23
11 ACQSRSSGGP 19

```

SULT 11
 G66984 AA66984 standard; peptide; 25 AA.
AAG66984;
29-OCT-2001 (first entry)
Mutant proprorcin linker region of PAP324 (MMP-9).
 Castor oil plant; ricin; preproricin; cyclostatin; antiinflammatory;
 antineuritic; antiarthritic; antiarteriosclerotic; neuroprotective;
 toxin; linker; protease-specific cleavage site; cancer;
 inflammatory disease; mutant; variant; matrix metalloproteinase 9; MMP-9
 UPA.

Arcinus Communis.
Synthetic.

WO200125267-A2.

12-APR-2001.

04-OCT-2000; 2000WO-CA001162.

04-OCT-1999; 99US-0157807P.
14-APR-2000; 2000US-0197469P.

(TWIN-) TWINSTRAND THERAPEUTICS INC.

The invention relates to a recombinant protein comprising an A chain of ricin-like toxin, a B chain of a ricin-like toxin and a heterologous polypeptide linker sequence that is specifically cleaved and activated by protease specific to cancer is useful for treating inflammation and cancer.

Claim 42: Fig 17C; 146pp; English.

WPI; 2001-300164/31.

inflammatory cells and cancer cells. The protein is useful for inhibiting or destroying cells expressing a specific protease, e.g., cancer cells found in T- and B-cell lymphoproliferative diseases, ovarian cancer, pancreatic cancer, head and neck cancer, squamous cell carcinoma, gastrointestinal cancer, breast cancer, prostate cancer or non-small cell lung cancer, or cells found in rheumatoid arthritis, atherosclerosis, Crohn's disease or central nervous system disease. The protein is useful for treating cancer and inflammation. The protein has the specificity for cells that contain a specific protease, including those of inflammatory disorders and cancer cells, without the need for a cell binding component. The present sequence is one of a number of variant linkers generated from the wild type preproricin linker. The variant linkers contain a Cleavage Recognition site for either matrix metalloproteinase 9 (MMP-9) or UPA

XX Sequence 25 AA;
 SQ Query Match 23.4%; Score 33; DB 4; Length 25;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 31996.
 XX microarray; gene expression analysis; probe;
 DE Human brain expressed exon; gene expression analysis; probe;
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX Homo sapiens.

RESULT 13
 AAM31181
 ID AAM31981 standard; protein; 25 AA.
 XX AC AAM31981;
 XX DT 17-OCT-2001 (first entry)
 DB Peptide #6018 encoded by probe for measuring placental gene expression.
 XX Probe; microarray; human; placenta; antenatal diagnosis;
 KW Genetic disorder.
 XX OS Homo sapiens.
 PN WO200157272-A2.
 XX DR 09-AUG-2001.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PT 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00623366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-4888900/53.
 XX DR WPI; 2001-4888900/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX PR Example 4; SEQ ID NO 31996; 658pp + Sequence Listing; English.
 XX PS The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX SQ Sequence 25 AA;
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632166.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX PR Claim 27; SEQ ID NO 322250; 654pp; English.
 XX PS The present invention relates to single exon nucleic acid probes (SENPs;
 CC see AAI31313-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XXX SQ Sequence 25 AA;
 XX AC AAM39154;
 XX DT 05-NOV-2001 (first entry)
 DB Human brain expressed single exon probe encoded protein SEQ ID NO: 31259.
 XX DE Human brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX OS Homo sapiens.

RESULT 14
 AAM71690
 ID AAM71690 standard; protein; 25 AA.
 XX AC AAM71690;
 XX DT 06-NOV-2001 (first entry)
 DB Human bone marrow expressed probe encoded protein SEQ ID NO: 31996.
 XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31996.
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX Homo sapiens.

RESULT 15
 AAM59154
 ID AAM59154 standard; protein; 25 AA.
 XX AC AAM59154;
 XX DT 05-NOV-2001 (first entry)
 DB Human brain expressed single exon probe encoded protein SEQ ID NO: 31259.
 XX DE Human brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX OS Homo sapiens.

RESULT 16
 AAM71690
 ID AAM71690 standard; protein; 25 AA.
 XX AC AAM71690;
 XX DT 09-AUG-2001.
 DB WO200157275-A2.

XX
 XX 30-JAN-2001; 2001WO-US000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00600408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234587P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024623.

XX
 PA (MOLE) MOLECULAR DYNAMICS INC.

XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR; 2001-483446/52.

XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 brain.

XX
 DS Example 4; SEQ ID NO 31259; 650pp + Sequence Listing; English.

XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.
 XX Sequence 25 AA;

Query Match 23.4%; Score 33; DB 4; Length 25;
 Best Local Similarity 40.0%; Pred No. 4.3e-03;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 8 DEGKRGDACEGDGG 22
 :|||:|||:
 Db 10 BEGMQGDEPDHNHGG 24

Search completed: February 26, 2004, 09:48:22
 Job time : 56 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:49:38 ; Search time 33 Seconds
(without alignments)

159.965 Million cell updates/sec

Title: US-09-909-348-5
Perfect score: 141
Sequence: 1 AGTRKPDGEGKRGDACEBGDSGGPPV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 2731

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AAI:
1: /cgns2_6/ptodata/2/pbpa/US07_PUBCOMB.pep/*
2: /cgns2_6/ptodata/2/pbpa/PC7_NEW_PUB.pep/*
3: /cgns2_6/ptodata/2/pbpa/US06_PUB.pep/*
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18: /cgns2_6/ptodata/2/pbpa/US60_PUBCOMB.pep/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	%
1	141	100.0	25	9 US-09-909-348-5	Sequence 5, Appli	
2	141	100.0	25	9 US-09-909-112-5	Sequence 5, Appli	
3	141	100.0	25	13 US-10-090-692-5	Sequence 5, Appli	
4	38	27.0	25	15 US-10-354-522A-1	Sequence 1, Appli	
5	36	25.5	25	9 US-09-864-761-37498	Sequence 37498, A	
6	33	23.4	25	9 US-09-864-761-43492	Sequence 43492, A	
7	31.5	22.3	25	14 US-10-250-066-233	Sequence 233, Appli	
8	31	22.0	25	10 US-09-832-455-75	Sequence 75, Appli	
9	31	22.0	25	10 US-09-922-756-1099	Sequence 1099, Ap	
10	31	22.0	25	14 US-10-133-128-205	Sequence 205, App	
11	31	22.0	25	14 US-10-289-660-205	Sequence 205, App	
12	31	22.0	25	16 US-10-233-471-1099	Sequence 1099, Ap	
13	31	22.0	25	16 US-10-233-493-1099	Sequence 1099, Ap	
14	30	21.3	25	10 US-09-943-767-598	Sequence 598, App	
15	30	21.3	25	13 US-10-036-869-7	Sequence 7, Appli	

RESULT 1
US-09-909-348-5
; Sequence 5, Application US/09909348
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; CROWDER, Roger S.
; APPLICANT: Stierenberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: 3033_1003-001
; CURRENT APPLICATION NUMBER: US/09/909-348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO: 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; US-09-909-348-5

Query Match 100.0%; Score 141; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.7e-12;
Matches 25; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 AGTRKPDGEGKRGDACEGDSGGPPV 25
Db 1 AGTRKPDGEGKRGDACEGDSGGPPV 25

RESULT 2
US-09-909-112-5
; Sequence 5, Application US/09909122

ALIGNMENTS

Sequence 598, App
Sequence 11, Appl
Sequence 409, App
Sequence 45944, A
Sequence 255, App
Sequence 219, App
Sequence 23, Appl
Sequence 3, Appl
Sequence 256, App
Sequence 3, Appl
Sequence 32, App
Sequence 31, App
Sequence 312, App
Sequence 314, App
Sequence 31, App
Sequence 45572, A
Sequence 322, App
Sequence 263, App
Sequence 362, App
Sequence 118, App
Sequence 28, App
Sequence 31, App
Sequence 118, App
Sequence 4, Appl
Sequence 31, App
Sequence 362, App
Sequence 26, App
Sequence 16, App
Sequence 15, App
Sequence 14, App
Sequence 13, App
Sequence 12, App
Sequence 11, App
Sequence 10, App
Sequence 9, App
Sequence 8, App
Sequence 7, App
Sequence 6, App
Sequence 5, App
Sequence 4, App
Sequence 3, App
Sequence 2, App
Sequence 1, App
Sequence 0, App

Patent No. US20020128202A1
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
 FILE REFERENCE: 3033.1002-001
 CURRENT APPLICATION NUMBER: US/09/909,122
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide fragment of Thrombin
 US-09-909-122-5

Query Match Score 141; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.7e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTRYKPDGKRGDAECDGSQQPFV 25
 Db 1 AGTRYKPDGKRGDAECDGSQQPFV 25

RESULT 3
 US-10-050-692-5
 Publication No. US2002010050692
 GENERAL INFORMATION:
 APPLICANT: Carney, Darrell H.
 APPLICANT: Crowther, Roger S.
 APPLICANT: Simmons, David J.
 APPLICANT: Yang, Jinping
 APPLICANT: Redin, William R.
 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
 FILE REFERENCE: 3033.1002-004
 CURRENT APPLICATION NUMBER: US/10/030,692
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 09/909,122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 60/219,300
 PRIOR FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fragment of human prothrombin
 US-10-050-692-5

Query Match Score 141; DB 13; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.7e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTRYKPDGKRGDAECDGSQQPFV 25
 Db 1 AGTRYKPDGKRGDAECDGSQQPFV 25

RESULT 4
 US-10-353-522A-1

Sequence 1, Application US/10353522A
 Publication No. US20030216296A1
 GENERAL INFORMATION:
 APPLICANT: Weigene Pharmaceuticals, Inc.
 APPLICANT: Park, Jong-Gu
 APPLICANT: Moon, Ik-Jae
 APPLICANT: Kim, Young-Cheol
 TITLE OF INVENTION: Peptide for Increasing Transfection Efficiency
 FILE REFERENCE: 57354-13USA
 CURRENT APPLICATION NUMBER: US/10/353,522A
 CURRENT FILING DATE: 2003-01-28
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 1
 LENGTH: 25
 TYPE: PRT
 ORGANISM: artificial
 FEATURE:
 OTHER INFORMATION: RGD-RGD-TatC-RGD-RGD
 US-10-353-522A-1

Query Match Score 38; DB 15; Length 25;
 Best Local Similarity 40.0%; Pred. No. 2.4e-02;
 Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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 Db 5 GDRKRRQRRRPQCGDRG 24

RESULT 5
 US-09-864-761-3749B
 Sequence 3749B, Application US/09864761
 Patent No. US20020048733A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wenhong
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670

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; PRIORITY APPLICATION NUMBER: PCT/US01/00663
; PRIORITY FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: US 60/234,687
; PRIORITY FILING DATE: 2000-09-21
; PRIORITY APPLICATION NUMBER: US 09/608,408
; PRIORITY FILING DATE: 2000-06-30
; PRIORITY APPLICATION NUMBER: US 09/774,203
; PRIORITY FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 37498
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011504.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.5
; OTHER INFORMATION: SWISSPROT HIT: P22857, EVALUATE 1.70e+00
; US-09-864-761-37498

Query Match Score 36; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 15 ACBDGDSGGP 23
Db 11 ACCQSRSGGP 19

RESULT 6
US-09-864-761-43492
; Sequence 43492, Application US/09864761
; PATENT No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US/09/864 761
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

Query Match Score 36; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 15 ACBDGDSGGP 23
Db 11 ACCQSRSGGP 19

RESULT 7
US-10-280-066-233
; Sequence 233, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pilliata, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedorra, Olga
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BI
; FILE REFERENCE: 2598-400951
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 233
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: 07902-DG12-20M-PP-BC-C5
; US-10-280-066-233

Query Match Score 31.5; DB 14; Length 25;
Best Local Similarity 52.9%; Pred. No. 1.1e+03;
Matches 9; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 AGTRYKPDDESKRGDAE 17

```

Db 10 AGFRLLVGRGDRGD-CE 25 US-09-962-756-1099

RESULT 8
 Sequence 75, Application US/09852455
 GENERAL INFORMATION:
 APPLICANT: BLUME, ARTHUR J.
 APPLICANT: GOLDSTEIN, NEIL
 APPLICANT: PILLUTLA, RENUKA
 APPLICANT: HSTAO, KU-CHUAN
 APPLICANT: PRENDERGAST, JOHN
 TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
 FILE REFERENCE: 2598-400US1
 CURRENT APPLICATION NUMBER: US/09/852,455
 CURRENT FILING DATE: 2001-05-19
 PRIOR APPLICATION NUMBER: 60/202,912
 PRIOR FILING DATE: 2000-05-09
 NUMBER OF SEQ ID NOS: 81
 SEQ ID NO: 75
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-852-455-75

Query Match Score 31; DB 10; Length 25;
 Best Local Similarity 75.0%; Pred. No. 2e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 GDSGCPFPV 25
 Db 2 GDGGGALV 9

RESULT 9
 Sequence 1019, Application US/09962756
 GENERAL INFORMATION:
 APPLICANT: PILLUTLA, RENUKA
 APPLICANT: BRISSETTE, RENEE
 APPLICANT: BLONE, ARTHUR J.
 APPLICANT: SCHAFER, LAIGE
 APPLICANT: BRANDT, JAKOB
 APPLICANT: GOLDSTEIN, NEIL I.
 APPLICANT: SPETZLER, JANE
 APPLICANT: OSTERGAARD, SOREN
 APPLICANT: HANSEN, PER HERTZ
 TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 FILE REFERENCE: 1878-405US1
 CURRENT APPLICATION NUMBER: US/09/962,756
 CURRENT FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: 09/1538,038
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/146,127
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 2227
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1099
 LENGTH: 25

Query Match Score 31; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 2e+03;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 10 GKRGAACEGDSGG 22
 Db 7 GGCGGGCGGGGG 19

RESULT 11
 Sequence 205, Application US/10289660
 GENERAL INFORMATION:
 APPLICANT: KOLKMAN, JOOST A.
 APPLICANT: STEMER, WILLIAM P.C.
 APPLICANT: GOVINDARAJAN, SRIDHAR
 TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
 FILE REFERENCE: 0319-510US
 CURRENT APPLICATION NUMBER: US/10/289,660
 CURRENT FILING DATE: 2003-11-06
 PRIOR APPLICATION NUMBER: 10/133,128

OTHER INFORMATION: Unknown amino acid; translation read-through at TGA stop codon

```

Prior Filing Date: 2002-04-26
Prior Application Number: 60/374,107
Prior Filing Date: 2002-04-18
Prior Application Number: 60/333,359
Prior Filing Date: 2001-11-26
Prior Application Number: 60/337,209
Prior Filing Date: 2001-11-19
Prior Application Number: 60/286,823
Prior Filing Date: 2001-04-26
Number of SEQ ID NOS: 244
Software: PatentIn Ver. 2.1
SEQ ID NO: 205
Length: 25
Type: PRT
Organism: Artificial Sequence
Feature: Other Information: Description of Artificial Sequence: Synthetic
Feature: Other Information: Peptide Linker
Name/Key: misc_feature
Location: (1)-(12)
Other Information: This region may vary in length from 1-12 residues,
Other Information: 3-9 residues, 4-8 residues or 4-7 residues
Feature: Name/Key: misc_feature
Location: (14)-(25)
Other Information: This region may vary in length from 1-12 residues,
Other Information: 3-9 residues, 4-8 residues or 4-7 residues
US-10-289-660-205

Query Match Score 22.0%; Best Local Similarity 46.2%; Matches 6;保守性 0; Mismatches 7; Indels 0; Gaps 0;
Qy 10 GRGDACEGDSGG 22
Db 7 G3GGGGGGGGGGG 19

RESULT 12
US-10-253-471-1099
Publication No. US03036190A1
General Information:
Applicant: PILLUTLA, RENUKA et al.
Title of Invention: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
File Reference: 1878-4057
Current Filing Date: 2002-09-24
Prior Filing Date: 2001-09-24
Prior Application Number: 09/538,038
Prior Filing Date: 2000-03-29
Prior Filing Date: 1998-09-02
Number of SEQ ID NOS: 2227
Software: PatentIn Ver. 2.1
SEQ ID NO: 1099
Length: 25
Type: PRT
Organism: Artificial Sequence
Feature: Other Information: Description of Artificial Sequence: Synthetic
Feature: Other Information: Peptide
Name/Key: MOD_RES
Location: (13)
Other Information: Unknown amino acid; translation read-through at
Other Information: TGA stop codon
US-10-253-471-1099

Query Match Score 22.0%; Best Local Similarity 57.1%; Matches 4;保守性 0; Mismatches 3; Indels 0; Gaps 0;
Qy 18 GDSGGPF 24
Db 16 GEAGCPY 22

RESULT 13
US-10-253-493-1099
Sequence 1099, Application US/10253493
Publication No. US20040023887A1
General Information:
Applicant: PILLUTLA, RENUKA et al.
Title of Invention: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
File Reference: 1878-4056
Current Application Number: US/10/253,493
Current Filing Date: 2002-09-24
Prior Application Number: 09/962,756
Prior Filing Date: 2001-09-24
Prior Application Number: 09/538,038
Prior Filing Date: 2000-03-29
Prior Application Number: 09/146,127
Prior Filing Date: 1998-09-02
Number of SEQ ID NOS: 2227
Software: PatentIn Ver. 2.1
SEQ ID NO: 1099
Length: 25
Type: PRT
Organism: Artificial Sequence
Feature: Other Information: Description of Artificial Sequence: Synthetic
Feature: Other Information: Peptide
Name/Key: MOD_RES
Location: (13)
Other Information: Unknown amino acid; translation read-through at
Other Information: TGA stop codon
US-10-253-493-1099

Query Match Score 22.0%; Best Local Similarity 57.1%; Matches 4;保守性 0; Mismatches 3; Indels 0; Gaps 0;
Qy 18 GDSGGPF 24
Db 16 GEAGCPY 22

RESULT 14
US-09-933-767-598
Sequence 598, Application US/09933767
Publication No. US20030181692A1
General Information:
Applicant: Ni et al.
Title of Invention: 207 Human Secreted Proteins
File Reference: P2007P2
Current Application Number: US/09/933,767
Current Filing Date: 2001-08-22
Prior Application Number: PCT/US01/05614
Prior Filing Date: 2001-02-21
Prior Application Number: 60/184,836
Prior Filing Date: 2000-02-24
Prior Application Number: 60/193,170
Prior Filing Date: 2000-03-29
Prior Application Number: PCT/US01/05614
Prior Filing Date: 1998-12-04
Prior Application Number: PCT/US98/11422
Prior Filing Date: 1998-06-04
Prior Application Number: 60/048,885
Prior Filing Date: 1997-06-05
Prior Application Number: 60/049,375
Prior Filing Date: 1997-06-06
Prior Application Number: 60/048,881

Query Match Score 22.0%; Best Local Similarity 57.1%; Matches 4;保守性 0; Mismatches 3; Indels 0; Gaps 0;
Qy 18 GDSGGPF 24
Db 16 GEAGCPY 22

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PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 880
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 896
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 895
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049, 020
PRIOR FILING DATE: 1997-06-06
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PRIOR FILING DATE: 1997-06-06
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PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 971
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 964
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PRIOR APPLICATION NUMBER: 60/048, 901
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 902
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 915
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049, 019
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 972
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 916
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049, 373
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 875
PRIOR FILING DATE: 1997-06-06
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PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 883
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PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 949
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 962
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 897
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 898
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 877
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048, 878
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068, 054
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 064
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 053
PRIOR FILING DATE: 1997-12-18

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PRIORITY APPLICATION NUMBER: 60/070,923
PRIORITY FILING DATE: 1997-12-18
PRIORITY APPLICATION NUMBER: 60/073,160
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,159
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,165
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,164
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/085,925
PRIORITY FILING DATE: 1998-05-18
PRIORITY APPLICATION NUMBER: 60/085,921
PRIORITY FILING DATE: 1998-05-18
PRIORITY APPLICATION NUMBER: 60/085,923
PRIORITY FILING DATE: 1998-05-18
PRIORITY APPLICATION NUMBER: 60/085,922
PRIORITY FILING DATE: 1998-05-18
PRIORITY APPLICATION NUMBER: 60/092,921
PRIORITY FILING DATE: 1998-07-15
PRIORITY APPLICATION NUMBER: 60/094,657
PRIORITY FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1245
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 598
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
US-09-933-767-598

Query Match          Score 30; DB:10; Length: 25;
Best Local Similarity        42.9%; Pred. No: 2.8e+03;
Matches      6; Conservative   3; Mismatches 5; Indels 0; Gaps 0;

QY          9 EGKRGDAECDGSGG 22
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Db          4 EGKRGKACKNCTCG 17

RESULT 15
US-10-036-869-7
Sequence 7, Application US/10036869
Publication No. US2000101516A1
GENERAL INFORMATION
APPLICANT: Mission, James A.
TITLE OF INVENTION: CARRIER DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOTICENIC PEPTIDES AND THEIR USE IN GENE
THERAPY

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
    MEDIUM: TYPE: FLOPPY disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA: Patient In Release #1.0, version #1.25
    APPLICATION NUMBER: US/10/036,869
    FILING DATE: 29-No.-US/00201516A1-2001
    CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/985,526
    FILING DATE: Unknown
    APPLICATION NUMBER: US/08/608,845
    FILING DATE: 16-JUL-1996
    ATTORNEY/AGENT INFORMATION:
        NAME: McHarrow Jr., Robert G
    TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (302) 658-9141
TELEFAX: (302) 655-5613
INFORMATION FOR SEQ ID NO: ;
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-036-859-7:

Query Match Score 30; DB 13; Length 25;
Best Local Similarity 40.0%; Pred. No. 2.8e+0;
Matches 8; Conservative 2; Mismatches 10; Indels 0;
Gaps 0;
QY 2 GTRYKPDGKGKRGACEGSG 21
|:| | | :| | |
Db 4 GSRGKSYIGSRGKSYIGSRG 23

Search completed: February 26, 2004, 09:54:54
Job time : 15 secs

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Title: US-09-909-348-5
Perfect score: 141

Sequence: 1 AGTRYKPDEGKRGDACEGDSGGPFFV 25

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searched: 389414 seen: 51625971 residues

total number of hits satisfying chosen parameters: 2669

Minimum DB seq length: 25

maximum DB seq length: 25

post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Issued Patents AA: *

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pred. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, and is derived by analysis of the total scores distributed.

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2	30	21.3		25	4	US-08-900	-30-29
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4	29	20.6		25	4	US-08-473	475A-7
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8	29	20.6		25	3	US-08-454	-998-24
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17	27.5	19.5		25	1	US-08-502	989-22
18	27.5	19.5		25	1	US-08-502	-909-14
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20	27.5	19.5		25	5	PCT-US94-	53355-12
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22	27.5	19.5		25	5	PCT-US94-	53355-20
23	27.5	19.5		25	5	PCT-US94-	53355-21
24	27.5	19.5		25	5	PCT-US94-	53355-22
25	27	19.1		25	1	US-08-457	-229-3
26	27	19.1		25	2	US-08-457	487-3
27	27	19.1		25	2	US-08-457	519-3

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RESULT 1
US-08-985-526-7
; Sequence 7, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connally, Bove, Lodge, & Hertz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608, 845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-7
; Query Match Score 30; DB 3; Length 25;
; Best Local Similarity 40.0%; Pred. No. 8.2e+02;
; Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
; 2 GTRYPKDPDKRDKDACEGDSG 21
; 4 GSPCKSYTSPAKSVPKSGPQG 23

```

RESULT 2
US-08-900-230-29
Sequence 29, Application US/08900230
Patient No. 6129197
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A.
TITLE OF INVENTION: DNA ENCODING GALANNEAL3 RECEPTORS AND NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEES: Cooper & Dunham LLP
STREET: 1185 Avenue of The Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,230
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: S2241-C/JPW/ADM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No
HYPOTHETICAL: No
ANTI-SENSE: No
US-08-900-230-29

Query Match 21.3%; Score 30; DB 4; Length 25;
Best Local Similarity 46.2%; Pred. No. 8.2e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 10 GKGDAEGDSSG 22
Db 5 GCAGAACTGTGTAG 17

RESULT 3
US-09-205-558-558
Sequence 59, Application US/09205258
Patient No. 6555174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1997-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ_ID NO 598
; LENGTH: 25

TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-203-258-598

Query Match 21.3%; Score 30; DB 4; Length 25;
 Best Local Similarity 42.9%; Pred. No. 8.2e+02;
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 9 EGKRCDAEGDGG 22
 Db 4 EGKRKAKCNCCTCG 17

RESULT 4
 US-08-473-475A-7
 Sequence 7, Application US/08473475A

GENERAL INFORMATION:
 PATENT NO. 5843450
 APPLICANT: DAWSON, GEORGE
 APPLICANT: BRIDON, DOMINIQUE P.
 APPLICANT: SCHROEDER-POLIAK, PAMELLA A.
 APPLICANT: KNIGGE, MARK F.
 APPLICANT: JAFFE, KEVEE

TITLE OF INVENTION: HEPATITIS GB VIRUS SYNTHETIC PEPTIDES

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 ZIP: 60064

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/473,475A
 FILING DATE:
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: FORENSKI, PRISCILLA E.
 REGISTRATION NUMBER: 23206
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-937-2623

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-473-475A-7

Query Match 20.6%; Score 29; DB 2; Length 25;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 7 PDGKRGDAEGDS 20
 Db 10 PESLQRSDPLEGPS 23

RESULT 5
 US-08-263-911-5
 Sequence 5, Application US/08263911
 PATENT NO. 5877291
 GENERAL INFORMATION:
 APPLICANT: Mees, Peter S

APPLICANT: Gourlie, Brian B
 TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Duane C. Ulmer
 STREET: P.O. Box 1967
 CITY: Midland
 STATE: MI
 COUNTRY: US
 ZIP: 48641-1967
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/263,911
 FILING DATE: 21-JUN-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,263
 FILING DATE: 11-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Ulmer, Duane C
 REGISTRATION NUMBER: 34,941
 REFERENCE/DOCKET NUMBER: C-41,014
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (517) 636-8104
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-263-911-5

Query Match 20.6%; Score 29; DB 2; Length 25;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KPDEGKRGDAEGDS 20
 Db 7 KRDAARKDDAKRDKDA 21

RESULT 6
 US-09-184-658-42
 Sequence 42, Application US/09184658
 PATENT NO. 6030792
 GENERAL INFORMATION:
 APPLICANT: Otterness, Ivan G.
 APPLICANT: Mezes, Peter S.
 APPLICANT: Downs, James T.
 APPLICANT: Johnson, Kimberly S.
 TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
 Title of Invention: Biological Media
 FILE REFERENCE: PC946-A
 CURRENT APPLICATION NUMBER: US/09/184,658
 CURRENT FILING DATE: 1997-11-02
 EARLIER APPLICATION NUMBER: 60/065,423
 NUMBER OF SEQ ID NOS: 69
 SEQ ID NO 42
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Single chain
 OTHER INFORMATION: Antibody linker sequence.
 US-09-184-658-42

Query Match 20.6%; Score 29; DB 3; Length 25;

Best Local Similarity 40.0%; Pred. No. 1.1e+03; 1; Mismatches 8; Indels 0; Gaps 0;

Matches 6; Conservative 3; Mismatches 6; Indexes 0; Gaps 0;

Oy 6 KPDEGKRGDACEGDS 20
Db 7 KKDAAKKDDAKKDDA 21

RESULT 10

US-07-935-595-31

Sequence 31, Application US/07935695

Patent No. 6339507

GENERAL INFORMATION:

APPLICANT: Mezes, Peter S.

APPLICANT: Richard, Ruth A.

APPLICANT: Affholter, Joseph A.

TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides

CURRENT APPLICATION NUMBER: US/07/935,695

CURRENT FILING DATE: 1992-08-21

PRIOR APPLICATION NUMBER: US 08/463,903

PRIOR FILING DATE: 1993-06-05

NUMBER OF SEQ ID NOS: 102

SEQ ID NO: 31

LENGTH: 25

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: UNIHOPE linker

LOCATION: 1..25

OTHER INFORMATION: :

US-07-935-695-31

Query Match Score 29; DB 4; Length 25;

Best Local Similarity 40.0%; Pred. No. 1.1e+03; 3; Mismatches 6; Indels 0; Gaps 0;

Matches 6 KPDEGKRGDACEGDS 20
Db 7 KKDAAKKDDAKKDDA 21

RESULT 11

US-09-504-262D-42

Sequence 42, Application US/0904262D

Patent No. 6642007

GENERAL INFORMATION:

APPLICANT: Pfizer Inc.

APPLICANT: Saltarelli, Mary J.

APPLICANT: Johnson, Kimberly S.

APPLICANT: Oettmers, Ivan G.

TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine

FILE REFERENCE: PC11189GR - CIP OF PC946A

CURRENT APPLICATION NUMBER: US/09/504,262D

CURRENT FILING DATE: 2000-02-15

NUMBER OF SEQ ID NOS: 70

SEQ ID NO: 42

LENGTH: 25

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer for PCR-SOE

NAME/KEY: misc feature

OTHER INFORMATION: Description of Artificial Sequence: Single chain antibody linker

OTHER INFORMATION: sequence.

US-09-504-262D-42

Query Match Score 29; DB 4; Length 25;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;

LOCATION: 24
 OTHER INFORMATION: /note= "Xaa at location 24 is
 cyclohexylalanine"
 FEATURE: Modified-site
 NAME/KEY: LOCATION: 11
 OTHER INFORMATION: /note= "Xaa at location 11 is
 cyclohexalanine"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 25
 OTHER INFORMATION: /note= "Xaa at location 25 is
 glutamic acid in the D-configuration"
 US-08-502-989-1

Query Match 19.5%; Score 27.5; DB 1; Length 25;
 Best Local Similarity 50.0%; Pred. No. 1. 9e+03;
 Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 OTHER INFORMATION: and is sulfide bonded to D-Cys at location 6"

Qy 6 KPDEGKRGDACEGD 19
 Db 3 RPGXG-RGDXPxGd 15

RESULT 13 - US-08-502-989-12

Sequence 12, Application US/08502989
 Patent No. 5681925
 GENERAL INFORMATION:
 APPLICANT: Broersma, Robert J
 APPLICANT: Owen, Thomas J
 APPLICANT: Krstenansky, John L
 TITLE OF INVENTION: TRIFUNCTIONAL ANTITHROMBIN AND
 TITLE OF INVENTION: ANTIPLATELET PEPTIDES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merrell Dow Pharmaceuticals Inc.
 STREET: 2110 E. Galbraith Road, P.O. Box 156300
 CITY: Cincinnati
 STATE: Ohio
 COUNTRY: USA
 ZIP: 45215-6300
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/502,989
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/076,066
 FILING DATE: 11-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Boudreux, William R
 REGISTRATION NUMBER: 35,796
 REFERENCE/DOCKET NUMBER: M01696 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 513/948-6566
 TELEX: 214320
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "Xaa at location 1 is
 phenylalanine in the D-configuration"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: /note= "Xaa at location 6 is D-Cys
 and is sulfide bonded to D-Cys at location 13"
 OTHER INFORMATION: and is sulfide bonded to D-Cys at location 6"

FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: /note= "Xaa at location 11 is
 cyclohexalanine"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 13
 OTHER INFORMATION: /note= "Xaa at location 13 is D-Cys
 and is sulfide bonded to D-Cys at location 6"

Query Match 19.5%; Score 27.5; DB 1; Length 25;
 Best Local Similarity 50.0%; Pred. No. 1. 9e+03;
 Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 OTHER INFORMATION: and is sulfide bonded to D-Cys at location 6"

Qy 6 KPDEGKRGDACEGD 19
 Db 3 RPGXG-RGDXPxGd 15

RESULT 14 - US-08-502-989-13

Sequence 13, Application US/08502989
 Patent No. 5681925
 GENERAL INFORMATION:
 APPLICANT: Boersma, Robert J
 APPLICANT: Owen, Thomas J
 APPLICANT: Krstenansky, John L
 TITLE OF INVENTION: TRIFUNCTIONAL ANTITHROMBIN AND
 TITLE OF INVENTION: ANTIPLATELET PEPTIDES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merrell Dow Pharmaceuticals Inc.
 STREET: 2110 E. Galbraith Road, P.O. Box 156300
 CITY: Cincinnati
 STATE: Ohio
 COUNTRY: USA
 ZIP: 45215-6300
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/502,989
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/076,066
 FILING DATE: 11-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Boudreux, William R
 REGISTRATION NUMBER: 35,796
 REFERENCE/DOCKET NUMBER: M01696 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 513/948-6566
 TELEX: 214320
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "Xaa at location 1 is
 phenylalanine in the D-configuration"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: /note= "Xaa at location 6 is D-Cys
 and is sulfide bonded to D-Cys at location 13"
 OTHER INFORMATION: and is sulfide bonded to D-Cys at location 6"

TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "Xaa at location 1 is phenylalanine in the D-configuration"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: /note= "Xaa at location 6 is cysteine in the D-configuration"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: /note= "Xaa at location 11 is norleucine"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 13
 OTHER INFORMATION: /note= "Xaa at location 13 is penicillamine in the D-configuration"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 24
 OTHER INFORMATION: /note= "Xaa at location 24 is cyclohexylalanine"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 25
 OTHER INFORMATION: /note= "Xaa at location 25 is glutamic acid in the D-configuration"
 US-08-502-989-13
 Query Match 15
 Best Local Similarity 50.0% Score 27.5% DB 1; Length 25;
 Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 Qy 6 KPDEGRGRDAGEGKD 19
 Db 3 RPGXG-RGDGXGD 15
 RESULT 15
 US-08-502-989-20
 / Sequence 20, Application US/08502989
 / Patent No. 5681925
 / GENERAL INFORMATION:
 / APPLICANT: Broersma, Robert J
 / APPLICANT: Owen, Thomas J
 / APPLICANT: Kravtansky, John L
 / TITLE OF INVENTION: TRIFUNCTIONAL ANTITHROMBIN AND NUMBER OF SEQUENCES: 22
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Merrell Dow Pharmaceuticals Inc.
 / STREET: 2110 E. Galbraith Road, P.O. Box 156300
 / CITY: Cincinnati
 / STATE: Ohio
 / COUNTRY: USA
 / ZIP: 45215-6300
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/502-989
 / FILING DATE:
 / CLASSIFICATION: 514
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/076,066
 / FILING DATE: 11-JUN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Boudreax, William R
 REGISTRATION NUMBER: 35,796
 REFERENCE/DOCKET NUMBER: MD1696 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 513/948-6566
 TELEFAX: 513/948-7961 OR 4681
 TELEX: 214320
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "Xaa at location 1 is phenylglycine in the D-configuration"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: /note= "Xaa at location 6 is D-Cys
 OTHER INFORMATION: sulfide bonded to D-Cys at location 13"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: /note= "Xaa at location 11 is norleucine"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 13
 OTHER INFORMATION: /note= "Xaa at location 13 is D-Cys
 OTHER INFORMATION: sulfide bonded to D-Cys at location 6"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 24
 OTHER INFORMATION: /note= "Xaa at location 24 is cyclohexylalanine"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 25
 OTHER INFORMATION: /note= "Xaa at location 25 is glutamic acid in the D-configuration"
 US-08-502-989-20
 Query Match 19.5% Score 27.5% DB 1; Length 25;
 Best Local Similarity 50.0% Pred. No. 1.9e+03; Mismatches 5; Indels 1; Gaps 1;
 OTHER INFORMATION: /note= "Xaa at location 25 is glutamic acid in the D-configuration"
 US-08-502-989-20
 Query Match 19.5% Score 27.5% DB 1; Length 25;
 Best Local Similarity 50.0% Pred. No. 1.9e+03; Mismatches 5; Indels 1; Gaps 1;
 OTHER INFORMATION: /note= "Xaa at location 24 is cyclohexylalanine"
 US-08-502-989-20
 Qy 6 KPDEGRGRDAGEGKD 19
 Db 3 RPGXG-RGDGXGD 15
 Search completed: February 26, 2004, 09:50:42
 Job time : 24 secs